1441

CGTGATGCCTGCACCTATGCCACAGCCCTCAATGTAGCCAGCCTGAGTGTGGAGC
GCTAC

481 R D A C T Y A T A L N V A S L S V E R Y

1501

TTGGCCATCTGCCATCCCTTCAAGGCCAAGACCCTCATGTCCCGCAGCCGCACCA
AGAAA

501 L A I C H P F K A K T L M S R S R T K K

1561

TTCATCAGTGCCATATGGCTAGCTTCGGCGCTGCTGGCTATACCCATGCTTTTCAC
CATG

521 F I S A I W L A S A L L A I P M L F T M

1621

GGCCTGCAGAACCGCAGTGGTGACGGCACGCACCCTGGCGGCCTGGTGTGCACAC
CCATT

541 G L Q N R S G D G T H P G G L V C T P I

1681

GTGGACACAGCCACTGTCAAGGTCGTCATCCAGGTTAACACCTTCATGTCCTTCCT
GTTT

561 V D T A T V K V V I Q V N T F M S F L F

1741

CCCATGTTGGTCATCTCCATCCTAAACACCGTGATTGCCAACAAACTGACAGTCAT
GGTG

581 P M L V I S I L N T V I A N K L T V M V

1801

CACCAGGCCGCCGAGCAGGGCCGAGTGTGCACCGTGGGCACACACAACGGTTTAG
AGCAC

601 H Q A A E Q G R V C T V G T H N G L E H

1861

AGCACGTTCAACATGACCATCGAGCCGGGTCGTGTCCAGGCCCTGCGCCACGGAG
TCCTC

621 S T F N M T I E P G R V Q A L R H G V L

1921

GTCTTACGTGCTGTGGTCATTGCCTTTGTGGTCTGCTGGCTGCCCTACCACGTGCG
ACGC

641 V L R A V V I A F V V C W L P Y H V R R

1981

CTGATGTTCTGCTATATCTCGGATGAACAGTGGACTACGTTCCTCTTCGATTTCTA
CCAC

661 L M F C Y I S D E Q W T T F L F D F Y H

2041

TATTTCTACATGCTAACCAACGCTCTCTTCTACGTCAGCTCCGCCATCAATCCCAT
CCTC

681 Y F Y M L T N A L F Y V S S A I N P I L

2101

TACAACCTGGTCTCCGCCAACTTCCGCCAGGTCTTTCTGTCCACGCTGGCCTGCCT
TTGT

701 Y N L V S A N F R Q V F L S T L A C L C

2161

CCTGGGTGGCGCCACCGCCGAAAGAAGAGGCCAACGTTCTCCAGGAAGCCCAACA
GCATG

721 P G W R H R R K K R P T F S R K P N S M

NotI +2 TrxA

2221

TCCAGCAACCATGCCTTTTCCACCAGCGCCACCCGGGAGACCCTGTACgcggccgcaA
GC

741 S S N H A F S T S A T R E T L Y A A A S

2281

GATAAAATTATTCACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGG
ACGGG

761 D K I I H L T D D S F D T D V L K A D G

2341
GCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCC
CGATT

781 A I L V D F W A E W C G P C K M I A P I

2401
CTGGATGAAATCGCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAACA
TCGAT

801 L D E I A D E Y Q G K L T V A K L N I D

2461
CAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGC
TGTTC

821 Q N P G T A P K Y G I R G I P T L L L F

2521
AAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGA
AAGAG

841 K N G E V A A T K V G A L S K G Q L K E

NotI +2 Flag stop

2581
TTCCTCGACGCTAACCTGGCGgcggccgcaGATTATAAAGATGACGATGACAAATAAT
AA

861 F L D A N L A A A A D Y K D D D D K * *

KpnI

2641 GGTACC

SEQ ID NO.: 170

MalE (1-28) Factor Xa NTR (43-424) TrxA (2-109) FLAG

SalI +1 MalE leader (1-28)

1
gtcgacATGAAAATAAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACG
ATGATGTTT

1 M K I K T G A R I L A L S A L T T M M F

Factor Xa +43 NTR

61
TCCGCCTCGGCTCTCGCCAAAATCATCGAAGCCCGCACCTCGGAATCCGACACGG
CAGGG

21 S A S A L A K I I E A R T S E S D T A G

121

CCCAACAGCGACCTGGACGTGAACACTGACATTTATTCCAAGGTGCTGGTGACTG
CTATA

41 P N S D L D V N T D I Y S K V L V T A I

181

TACCTGGCACTCTTCGTGGTGGGCACTGTGGGCAACTCCGTGACAGCCTTCACTCT
AGCG

61 Y L A L F V V G T V G N S V T A F T L A

241

CGGAAGAAGTCACTGCAGAGCCTGCAGAGCACTGTGCATTACCACCTGGGCAGCC
TGGCA

81 R K K S L Q S L Q S T V H Y H L G S L A

301

CTGTCGGACCTGCTTATCCTTCTGCTGGCCATGCCCGTGGAGCTATACAACTTCAT
CTGG

101 L S D L L I L L L A M P V E L Y N F I W

361

GTACACCATCCCTGGGCCTTTGGGGACGCTGGCTGCCGTGGCTACTATTTCCTGCG
TGAT

121 V H H P W A F G D A G C R G Y Y F L R D

421

GCCTGCACCTATGCCACAGCCCTCAATGTAGCCAGCCTGAGTGTGGAGCGCTACT
TGGCC

141 A C T Y A T A L N V A S L S V E R Y L A

481

ATCTGCCATCCCTTCAAGGCCAAGACCCTCATGTCCCGCAGCCGCACCAAGAAAT
TCATC

161 I C H P F K A K T L M S R S R T K K F I

541

AGTGCCATATGGCTAGCTTCGGCGCTGCTGGCTATACCCATGCTTTTCACCATGGG
CCTG

181 S A I W L A S A L L A I P M L F T M G L

601

CAGAACCGCAGTGGTGACGGCACGCACCCTGGCGGCCTGGTGTGCACACCCATTG
TGGAC

201 Q N R S G D G T H P G G L V C T P I V D

661

ACAGCCACTGTCAAGGTCGTCATCCAGGTTAACACCTTCATGTCCTTCCTGTTTCC
CATG

221 T A T V K V V I Q V N T F M S F L F P M

721

TTGGTCATCTCCATCCTAAACACCGTGATTGCCAACAAACTGACAGTCATGGTGCA
CCAG

241 L V I S I L N T V I A N K L T V M V H Q

781

GCCGCCGAGCAGGGCCGAGTGTGCACCGTGGGCACACACAACGGTTTAGAGCACA
GCACG

261 A A E Q G R V C T V G T H N G L E H S T

841

TTCAACATGACCATCGAGCCGGGTCGTGTCCAGGCCCTGCGCCACGGAGTCCTCG
TCTTA

281 F N M T I E P G R V Q A L R H G V L V L

901

CGTGCTGTGGTCATTGCCTTTGTGGTCTGCTGGCTGCCCTACCACGTGCGACGCCT
GATG

301 R A V V I A F V V C W L P Y H V R R L M

961

TTCTGCTATATCTCGGATGAACAGTGGACTACGTTCCTCTTCGATTTCTACCACTA
TTTC

321 F C Y I S D E Q W T T F L F D F Y H Y F

1021

TACATGCTAACCAACGCTCTCTTCTACGTCAGCTCCGCCATCAATCCCATCCTCTA
CAAC

341 Y M L T N A L F Y V S S A I N P I L Y N

1081

CTGGTCTCCGCCAACTTCCGCCAGGTCTTTCTGTCCACGCTGGCCTGCCTTTGTCC
TGGG

361 L V S A N F R Q V F L S T L A C L C P G

1141

TGGCGCCACCGCCGAAAGAAGAGGCCAACGTTCTCCAGGAAGCCCAACAGCATGT
CCAGC

381 W R H R R K K R P T F S R K P N S M S S

NotI +2 TrxA

1201

AACCATGCCTTTTCCACCAGCGCCACCCGGGAGACCCTGTACgcggccgcaAGCGATA
AA

401 N H A F S T S A T R E T L Y A A A S D K

1261

ATTATTCACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGG
CGATC

421 I I H L T D D S F D T D V L K A D G A I

1321

CTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCT
GGAT

441 L V D F W A E W C G P C K M I A P I L D

1381

GAAATCGCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAACATCGATC
AAAAC

461 E I A D E Y Q G K L T V A K L N I D Q N

1441

CCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAA
AAAC

481 P G T A P K Y G I R G I P T L L L F K N

1501

GGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGT
TCCTC

501 G E V A A T K V G A L S K G Q L K E F L

NotI Flag stop KpnI

1561

GACGCTAACCTGGCAgcggccgcaGATTATAAAGATGACGATGACAAATAATAAGGTA
CC

521 D A N L A A A A D Y K D D D D K

SEQ ID NO.: 188

Human 2AR GS1 chimeric fusion

SalI +1 B2AR

1 GTCGACATGG GGCAACCCGG GAACGGCAGC GCCTTCTTGC TGGCACCCAA TGGAAGCCAT

61 GCGCCGGACC ACGACGTCAC GCAGCAAAGG GACGAGGTGT GGGTGGTGGG CATGGGCATC

121 GTCATGTCTC TCATCGTCCT GGCCATCGTG TTTGGCAATG TGCTGGTCAT CACAGCCATT

181 GCCAAGTTCG AGCGTCTGCA GACGGTCACC AACTACTTCA TCACTTCACT GGCCTGTGCT

241 GATCTGGTCA TGGGCCTAGC AGTGGTGCCC TTTGGGGCCG CCCATATTCT TATGAAAATG

301 TGGACTTTTG GCAACTTCTG GTGCGAGTTT TGGACTTCCA TTGATGTGCT GTGCGTCACG

361 GCCAGCATTG AGACCCTGTG CGTGATCGCA GTGGATCGCT ACTTTGCCAT TACTTCACCT

421 TTCAAGTACC AGAGCCTGCT GACCAAGAAT AAGGCCCGGG TGATCATTCT GATGGTGTGG

481 ATTGTGTCAG GCCTTAYCTC CTTCTTGCCC ATTCAGATGC ACTGGTACAG GGCCACCCAC

541 CAGGAAGCCA TCAACTGCTA TGCCAATGAG ACCTGCTGTG ACTTCTTCAC GAACCAAGCC

601 TATGCCATTG CCTCTTCCAT CGTGTCCTTC TACGTTCCCC TGGTGATCAT GGTCTTCGTC

661 TACTCCAGGG TCTTTCAGGA GGCCAAAAGG CAGCTCCAGA AGATTGACAA ATCTGAGGGC

721 CGCTTCCATG TCCAGAACCT TAGCCAGGTG GAGCAGGATG GGCGGACGGG GCATGGACTC

781 CGCAGATCTT CCAAGTTCTG CTTGAAGGAG CACAAAGCCC TCAAGACGTT AGGCATCATC

841 ATGGGCACTT TCACCCTCTG CTGGCTGCCC TTCTTCATCG TTAACATTGT GCATGTGATC

901 CAGGATAACC TCATCCGTAA GGAAGTTTAC ATCCTCCTAA ATTGGATAGG CTATGTCAAT

961 TCTGGTTTCA ATCCCCTTAT CTACTGCCGG AGCCCAGATT TCAGGATTGC CTTCCAGGAG

1021 CTTCTGTGCC TGCGCAGGTC TTCTTTGAAG GCCTATGGCA ATGGCTACTC CAGCAACGGC

1081 AACACAGGGG AGCAGAGTGG ATATCACGTG GAACAGGAGA AAGAAAATAA ACTGCTGTGT

1141 GAAGACCTCC CAGGCACGGA AGACTTTGTG GGCCATCAAG GTACTGTGCC TAGCGATAAC

Last B2AR Linker sequence

1201 ATTGATTCAC AAGGGAGGAA TTGTAGTACA AATGACTCAC TGCTAGAGCG TGGCCAGACG

PstI XhoI +2 GS1 alpha

1261 GTCACCAACC TGCAGCTCGA GGGCTGCCTC GGGAACAGTA AGACCGAGGA CCAGCGCAAC

1321 GAGGAGAAGG CGCAGCGTGA GGCCAACAAA AAGATCGAGA AGCAGCTGCA GAAGGACAAG

1381 CAGGTCTACC GGGCCACGCA CCGCCTGCTG CTGCTGGGTG CTGGAGAATC TGGTAAAAGC

1441 ACCATTGTGA AGCAGATGAG GATCCTGCAT GTTAATGGGT TTAATGGAGA CAGTGAGAAG

1501 GCAACCAAAG TGCAGGACAT CAAAAACAAC CTGAAAGAGG CGATTGAAAC CATTGTGGCC

1561 GCCATGAGCA ACCTGGTGCC CCCCGTGGAG CTGGCCAACC CCGAGAACCA GTTCAGAGTG

1621 GACTACATCC TGAGTGTGAT GAACGTGCCT GACTTTGACT TCCCTCCCGA ATTCTATGAG

1681 CATGCCAAGG CTCTGTGGGA GGATGAAGGA GTGCGTGCCT GCTACGAACG CTCCAACGAG

1741 TACCAGCTGA TTGACTGTGC CCAGTACTTC CTGGACAAGA TCGACGTGAT CAAGCAGGCT

1801 GACTATGTGC CGAGCGATCA GGACCTGCTT CGCTGCCGTG TCCTGACTTC TGGAATCTTT

1861 GAGACCAAGT TCCAGGTGGA CAAAGTCAAC TTCCACATGT TTGACGTGGG TGGCCAGCGC

1921 GATGAACGCC GCAAGTGGAT CCAGTGCTTC AACGATGTGA CTGCCATCAT CTTCGTGGTG

1981 GCCAGCAGCA GCTACAACAT GGTCATCCGG GAGGACAACC AGACCAACCG CCTGCAGGAG

2041 GCTCTGAACC TCTTCAAGAG CATCTGGAAC AACAGATGGC TGCGCACCAT CTCTGTGATC

2101 CTGTTCCTCA ACAAGCAAGA TCTGCTCGCT GAGAAAGTCC TTGCTGGGAA ATCGAAGATT

2161 GAGGACTACT TTCCAGAATT TGCTCGCTAC ACTACTCCTG AGGATGCTAC TCCCGAGCCC

2221 GGAGAGGACC CACGCGTGAC CCGGGCCAAG TACTTCATTC GAGATGAGTT TCTGAGGATC

2281 AGCACTGCCA GTGGAGATGG GCGTCACTAC TGCTACCCTC ATTTCACCTG CGCTGTGGAC

2341 ACTGAGAACA TCCGCCGTGT GTTCAACGAC TGCCGTGACA TCATTCAGCG CATGCACCTT

ClaI Stop XbaI Stem-loop

2401 CGTCAGTACG AGCTGCTCAT CGATTAATAA TCTAGAGGAT CCCCGCGCCC TCATCCGAAA

2461 GGGCG

SEQ ID NO.: 190

Human 2AR stop GS1 transcriptional fusion

PstI +1 B2AR

1 GTCGACATGG GGCAACCCGG GAACGGCAGC GCCTTCTTGC TGGCACCCAA TGGAAGCCAT

61 GCGCCGGACC ACGACGTCAC GCAGCAAAGG GACGAGGTGT GGGTGGTGGG CATGGGCATC

121 GTCATGTCTC TCATCGTCCT GGCCATCGTG TTTGGCAATG TGCTGGTCAT CACAGCCATT

181 GCCAAGTTCG AGCGTCTGCA GACGGTCACC AACTACTTCA TCACTTCACT GGCCTGTGCT

241 GATCTGGTCA TGGGCCTAGC AGTGGTGCCC TTTGGGGCCG CCCATATTCT TATGAAAATG

301 TGGACTTTTG GCAACTTCTG GTGCGAGTTT TGGACTTCCA TTGATGTGCT GTGCGTCACG

361 GCCAGCATTG AGACCCTGTG CGTGATCGCA GTGGATCGCT ACTTTGCCAT TACTTCACCT

421 TTCAAGTACC AGAGCCTGCT GACCAAGAAT AAGGCCCGGG TGATCATTCT GATGGTGTGG

481 ATTGTGTCAG GCCTTAYCTC CTTCTTGCCC ATTCAGATGC ACTGGTACAG GGCCACCCAC

541 CAGGAAGCCA TCAACTGCTA TGCCAATGAG ACCTGCTGTG ACTTCTTCAC GAACCAAGCC

601 TATGCCATTG CCTCTTCCAT CGTGTCCTTC TACGTTCCCC TGGTGATCAT GGTCTTCGTC

661 TACTCCAGGG TCTTTCAGGA GGCCAAAAGG CAGCTCCAGA AGATTGACAA ATCTGAGGGC

721 CGCTTCCATG TCCAGAACCT TAGCCAGGTG GAGCAGGATG GGCGGACGGG GCATGGACTC

781 CGCAGATCTT CCAAGTTCTG CTTGAAGGAG CACAAAGCCC TCAAGACGTT AGGCATCATC

841 ATGGGCACTT TCACCCTCTG CTGGCTGCCC TTCTTCATCG TTAACATTGT GCATGTGATC

901 CAGGATAACC TCATCCGTAA GGAAGTTTAC ATCCTCCTAA ATTGGATAGG CTATGTCAAT

961 TCTGGTTTCA ATCCCCTTAT CTACTGCCGG AGCCCAGATT TCAGGATTGC CTTCCAGGAG

1021 CTTCTGTGCC TGCGCAGGTC TTCTTTGAAG GCCTATGGCA ATGGCTACTC CAGCAACGGC

1081 AACACAGGGG AGCAGAGTGG ATATCACGTG GAACAGGAGA AAGAAAATAA ACTGCTGTGT

1141 GAAGACCTCC CAGGCACGGA AGACTTTGTG GGCCATCAAG GTACTGTGCC TAGCGATAAC

Last B2AR Linker

5 sequence

1201 ATTGATTCAC AAGGGAGGAA TTGTAGTACA AATGACTCAC TGCTAGAGCG TGGCCAGACG

PstI Stop SD XhoI +2 GS1 alpha

10 1261 GTCACCAACC TGCAGTAATA ATCAAGGAGG CCCTCGAGAT GGGCTGCCTC GGGAACAGTA

1321 AGACCGAGGA CCAGCGCAAC GAGGAGAAGG CGCAGCGTGA

15 GGCCAACAAA AAGATCGAGA

1381 AGCAGCTGCA GAAGGACAAG CAGGTCTACC GGGCCACGCA CCGCCTGCTG CTGCTGGGTG

1441 CTGGAGAATC TGGTAAAAGC ACCATTGTGA AGCAGATGAG GATCCTGCAT GTTAATGGGT

20 1501 TTAATGGAGA CAGTGAGAAG GCAACCAAAG TGCAGGACAT CAAAAACAAC CTGAAAGAGG

1561 CGATTGAAAC CATTGTGGCC GCCATGAGCA ACCTGGTGCC CCCCGTGGAG CTGGCCAACC

1621 CCGAGAACCA GTTCAGAGTG GACTACATCC TGAGTGTGAT

25 GAACGTGCCT GACTTTGACT

1681 TCCCTCCCGA ATTCTATGAG CATGCCAAGG CTCTGTGGGA GGATGAAGGA GTGCGTGCCT

1741 GCTACGAACG CTCCAACGAG TACCAGCTGA TTGACTGTGC CCAGTACTTC CTGGACAAGA

1801 TCGACGTGAT CAAGCAGGCT GACTATGTGC CGAGCGATCA GGACCTGCTT CGCTGCCGTG

1861 TCCTGACTTC TGGAATCTTT GAGACCAAGT TCCAGGTGGA CAAAGTCAAC TTCCACATGT

1921 TTGACGTGGG TGGCCAGCGC GATGAACGCC GCAAGTGGAT CCAGTGCTTC AACGATGTGA

1981 CTGCCATCAT CTTCGTGGTG GCCAGCAGCA GCTACAACAT GGTCATCCGG GAGGACAACC

2041 AGACCAACCG CCTGCAGGAG GCTCTGAACC TCTTCAAGAG CATCTGGAAC AACAGATGGC

2101 TGCGCACCAT CTCTGTGATC CTGTTCCTCA ACAAGCAAGA TCTGCTCGCT GAGAAAGTCC

2161 TTGCTGGGAA ATCGAAGATT GAGGACTACT TTCCAGAATT TGCTCGCTAC ACTACTCCTG

2221 AGGATGCTAC TCCCGAGCCC GGAGAGGACC CACGCGTGAC CCGGGCCAAG TACTTCATTC

2281 GAGATGAGTT TCTGAGGATC AGCACTGCCA GTGGAGATGG GCGTCACTAC TGCTACCCTC

2341 ATTTCACCTG CGCTGTGGAC ACTGAGAACA TCCGCCGTGT GTTCAACGAC TGCCGTGACA

ClaI Stop XbaI

2401 TCATTCAGCG CATGCACCTT CGTCAGTACG AGCTGCTCAT CGATTAATAA TCTAGAGGAT

Stem-loop

2461 CCCCGCGCCC TCATCCGAAA GGGCG

SEQ ID NO.: 192

Human GS1

XhoI

1
CTCGAGATGGGCTGCCTCGGGAACAGTAAGACCGAGGACCAGCGCAACGAGGAG AAGGCGCAGCGT

1 M G C L G N S K T E D Q R N E E K A Q R

61
GAGGCCAACAAAAAGATCGAGAAGCAGCTGCAGAAGGACAAGCAGGTCTACCGG GCCACG

21 E A N K K I E K Q L Q K D K Q V Y R A T

121

CACCGCCTGCTGCTGCTGGGTGCTGGAGAATCTGGTAAAAGCACCATTGTGAAGC
AGATG

41 H R L L L L G A G E S G K S T I V K Q M

181

AGGATCCTGCATGTTAATGGGTTTAATGGAGACAGTGAGAAGGCAACCAAAGTGC
AGGAC

61 R I L H V N G F N G D S E K A T K V Q D

241

ATCAAAAACAACCTGAAAGAGGCGATTGAAACCATTGTGGCCGCCATGAGCAACC
TGGTG

81 I K N N L K E A I E T I V A A M S N L V

301

CCCCCCGTGGAGCTGGCCAACCCCGAGAACCAGTTCAGAGTGGACTACATCCTGA
GTGTG

101 P P V E L A N P E N Q F R V D Y I L S V

361

ATGAACGTGCCTGACTTTGACTTCCCTCCCGAATTCTATGAGCATGCCAAGGCTCT
GTGG

121 M N V P D F D F P P E F Y E H A K A L W

421

GAGGATGAAGGAGTGCGTGCCTGCTACGAACGCTCCAACGAGTACCAGCTGATTG
ACTGT

141 E D E G V R A C Y E R S N E Y Q L I D C

481

GCCCAGTACTTCCTGGACAAGATCGACGTGATCAAGCAGGCTGACTATGTGCCGA
GCGAT

161 A Q Y F L D K I D V I K Q A D Y V P S D

541

CAGGACCTGCTTCGCTGCCGTGTCCTGACTTCTGGAATCTTTGAGACCAAGTTCCA
GGTG

181 Q D L L R C R V L T S G I F E T K F Q V

601

GACAAAGTCAACTTCCACATGTTTGACGTGGGTGGCCAGCGCGATGAACGCCGCA
AGTGG

201 D K V N F H M F D V G G Q R D E R R K W

661

ATCCAGTGCTTCAACGATGTGACTGCCATCATCTTCGTGGTGGCCAGCAGCAGCTA
CAAC

221 I Q C F N D V T A I I F V V A S S S Y N

721

ATGGTCATCCGGGAGGACAACCAGACCAACCGCCTGCAGGAGGCTCTGAACCTCT
TCAAG

241 M V I R E D N Q T N R L Q E A L N L F K

781

AGCATCTGGAACAACAGATGGCTGCGCACCATCTCTGTGATCCTGTTCCTCAACA
AGCAA

261 S I W N N R W L R T I S V I L F L N K Q

841

GATCTGCTCGCTGAGAAAGTCCTTGCTGGGAAATCGAAGATTGAGGACTACTTTC
CAGAA

281 D L L A E K V L A G K S K I E D Y F P E

901

TTTGCTCGCTACACTACTCCTGAGGATGCTACTCCCGAGCCCGGAGAGGACCCAC
GCGTG

301 F A R Y T T P E D A T P E P G E D P R V

961

ACCCGGGCCAAGTACTTCATTCGAGATGAGTTTCTGAGGATCAGCACTGCCAGTG
GAGAT

321 T R A K Y F I R D E F L R I S T A S G D

1021

GGGCGTCACTACTGCTACCCTCATTTCACCTGCGCTGTGGACACTGAGAACATCCG
CCGT

341 G R H Y C Y P H F T C A V D T E N I R R

1081

GTGTTCAACGACTGCCGTGACATCATTCAGCGCATGCACCTTCGTCAGTACGAGCT
GCTC

361 V F N D C R D I I Q R M H L R Q Y E L L

ClaI

ATCGAT

SEQ ID NO.: 193

Human GS2

XhoI

1

CTCGAGATGGGCTGCCTCGGGAACAGTAAGACCGAGGACCAGCGCAACGAGGAG
AAGGCGCAGCGT

1 M G C L G N S K T E D Q R N E E K A Q R

61

GAGGCCAACAAAAAGATCGAGAAGCAGCTGCAGAAGGACAAGCAGGTCTACCGG
GCCACG

21 E A N K K I E K Q L Q K D K Q V Y R A T

121

CACCGCCTGCTGCTGCTGGGTGCTGGAGAATCTGGTAAAAGCACCATTGTGAAGC
AGATG

41 H R L L L L G A G E S G K S T I V K Q M

181

AGGATCCTGCATGTTAATGGGTTTAATGGAGAGGGCGGCGAAGAGGACCCGCAGG
CTGCA

61 R I L H V N G F N G E G G E E D P Q A A

241

AGGAGCAACAGCGATGGTGAGAAGGCAACCAAAGTGCAGGACATCAAAAACAAC
CTGAAA

81 R S N S D G E K A T K V Q D I K N N L K

301

GAGGCGATTGAAACCATTGTGGCCGCCATGAGCAACCTGGTGCCCCCCGTGGAGC
TGGCC

101 E A I E T I V A A M S N L V P P V E L A

361

AACCCCGAGAACCAGTTCAGAGTGGACTACATCCTGAGTGTGATGAACGTGCCTG
ACTTT

121 N P E N Q F R V D Y I L S V M N V P D F

421

GACTTCCCTCCCGAATTCTATGAGCATGCCAAGGCTCTGTGGGAGGATGAAGGAG
TGCGT

141 D F P P E F Y E H A K A L W E D E G V R

481

GCCTGCTACGAACGCTCCAACGAGTACCAGCTGATTGACTGTGCCCAGTACTTCCT
GGAC

161 A C Y E R S N E Y Q L I D C A Q Y F L D

541

AAGATCGACGTGATCAAGCAGGCTGACTATGTGCCGAGCGATCAGGACCTGCTTC
GCTGC

181 K I D V I K Q A D Y V P S D Q D L L R C

601

CGTGTCCTGACTTCTGGAATCTTTGAGACCAAGTTCCAGGTGGACAAAGTCAACTT
CCAC

201 R V L T S G I F E T K F Q V D K V N F H

661

ATGTTTGACGTGGGTGGCCAGCGCGATGAACGCCGCAAGTGGATCCAGTGCTTCA
ACGAT

221 M F D V G G Q R D E R R K W I Q C F N D

721

GTGACTGCCATCATCTTCGTGGTGGCCAGCAGCAGCTACAACATGGTCATCCGGG
AGGAC

241 V T A I I F V V A S S S Y N M V I R E D

781

AACCAGACCAACCGCCTGCAGGAGGCTCTGAACCTCTTCAAGAGCATCTGGAACA
ACAGA

261 N Q T N R L Q E A L N L F K S I W N N R

841

TGGCTGCGCACCATCTCTGTGATCCTGTTCCTCAACAAGCAAGATCTGCTCGCTGA
GAAA

281 W L R T I S V I L F L N K Q D L L A E K

901

GTCCTTGCTGGGAAATCGAAGATTGAGGACTACTTTCCAGAATTTGCTCGCTACAC
TACT

301 V L A G K S K I E D Y F P E F A R Y T T

961

CCTGAGGATGCTACTCCCGAGCCCGGAGAGGACCCACGCGTGACCCGGGCCAAGT
ACTTC

321 P E D A T P E P G E D P R V T R A K Y F

1021

ATTCGAGATGAGTTTCTGAGGATCAGCACTGCCAGTGGAGATGGGCGTCACTACT
GCTAC

341 I R D E F L R I S T A S G D G R H Y C Y

1081

CCTCATTTCACCTGCGCTGTGGACACTGAGAACATCCGCCGTGTGTTCAACGACTG
CCGT

361 P H F T C A V D T E N I R R V F N D C R

ClaI

1141

GACATCATTCAGCGCATGCACCTTCGTCAGTACGAGCTGCTCATCGAT

381 D I I Q R M H L R Q Y E L L

SEQ ID NO.: 194

Human G q

XhoI

1

CTCGAGATGACTCTGGAGTCCATCATGGCGTGCTGCCTGAGCGAGGAGGCCAAGG
AAGCCCGGCGG

1 M T L E S I M A C C L S E E A K E A R R

61

ATCAACGACGAGATCGAGCGGCAGCTCCGCAGGGACAAGCGGGACGCCCGCCGG
GAGCTC

21 I N D E I E R Q L R R D K R D A R R E L

121

AAGCTGCTGCTGCTCGGGACAGGAGAGAGTGGCAAGAGTACGTTTATCAAGCAGA
TGAGA

41 K L L L L G T G E S G K S T F I K Q M R

181

ATCATCCATGGGTCAGGATACTCTGATGAAGATAAAAGGGGCTTCACCAAGCTGG
TGTAT

61 I I H G S G Y S D E D K R G F T K L V Y

241
CAGAACATCTTCACGGCCATGCAGGCCATGATCAGAGCCATGGACACACTCAAGA
TCCCA

81 Q N I F T A M Q A M I R A M D T L K I P

5

301
TACAAGTATGAGCACAATAAGGCTCATGCACAATTAGTTCGAGAAGTTGATGTGG
AGAAG

101 Y K Y E H N K A H A Q L V R E V D V E K

10

361
GTGTCTGCTTTTGAGAATCCATATGTAGATGCAATAAAGAGTTTATGGAATGATCC
TGGA

121 V S A F E N P Y V D A I K S L W N D P G

15

421
ATCCAGGAATGCTATGATAGACGACGAGAATATCAATTATCTGACTCTACCAAAT
ACTAT

141 I Q E C Y D R R R E Y Q L S D S T K Y Y

20

481
CTTAATGACTTGGACCGCGTAGCTGACCCTGCCTACCTGCCTACGCAACAAGATGT
GCTT

161 L N D L D R V A D P A Y L P T Q Q D V L

25

541

AGAGTTCGAGTCCCCACCACAGGGATCATCGAATACCCCTTTGACTTACAAAGTG
TCATT

181 R V R V P T T G I I E Y P F D L Q S V I

601

TTCAGAATGGTCGATGTAGGGGGCCAAAGGTCAGAGAGAAGAAAATGGATACACT
GCTTT

201 F R M V D V G G Q R S E R R K W I H C F

661

GAAAATGTCACCTCTATCATGTTTCTAGTAGCGCTTAGTGAATATGATCAAGTTCT
CGTG

221 E N V T S I M F L V A L S E Y D Q V L V

721

GAGTCAGACAATGAGAACCGAATGGAGGAAAGCAAGGCTCTCTTTAGAACAATTA
TCACA

241 E S D N E N R M E E S K A L F R T I I T

781

TACCCCTGGTTCCAGAACTCCTCGGTTATTCTGTTCTTAAACAAGAAAGATCTTCT
AGAG

261 Y P W F Q N S S V I L F L N K K D L L E

841

GAGAAAATCATGTATTCCCATCTAGTCGACTACTTCCCAGAATATGATGGACCCC
AGAGA

281 E K I M Y S H L V D Y F P E Y D G P Q R

901

GATGCCCAGGCAGCCCGAGAATTCATTCTGAAGATGTTCGTGGACCTGAACCCAG
ACAGT

301 D A Q A A R E F I L K M F V D L N P D S

961

GACAAAATTATCTACTCCCACTTCACGTGCGCCACAGACACCGAGAATATCCGCT
TTGTC

321 D K I I Y S H F T C A T D T E N I R F V

ClaI

1021

TTTGCTGCCGTCAAGGACACCATCCTCCAGTTGAACCTGAAGGAGTACAATCTGG
TCATCGAT

341 F A A V K D T I L Q L N L K E Y N L V

SEQ ID NO.: 195

Human Gi

XhoI

1

CTCGAGATGGGCTGCACCGTGAGCGCCGAGGACAAGGCGGCGGCCGAGCGCTCTA
AGATGATCGAC

1 M G C T V S A E D K A A A E R S K M I D

61

AAGAACCTGCGGGAGGACGGAGAGAAGGCGGCGCGGGAGGTGAAGTTGCTGCTG
TTGGGT

21 K N L R E D G E K A A R E V K L L L L G

121

GCTGGGGAGTCAGGGAAGAGCACCATCGTCAAGCAGATGAAGATCATCCACGAG
GATGGC

41 A G E S G K S T I V K Q M K I I H E D G

181

TACTCCGAGGAGGAATGCCGGCAGTACCGGGCGGTTGTCTACAGCAACACCATCC
AGTCC

61 Y S E E E C R Q Y R A V V Y S N T I Q S

241

ATCATGGCCATTGTCAAAGCCATGGGAAACCTGCAGATCGACTTTGCCGACCCCT
CCAGA

81 I M A I V K A M G N L Q I D F A D P S R

301

GCGGACGACGCCAGGCAGCTATTTGCACTGTCCTGCACCGCCGAGGAGCAAGGCG
TGCTC

101 A D D A R Q L F A L S C T A E E Q G V L

361

CCTGATGACCTGTCCGGCGTCATCCGGAGGCTCTGGGCTGACCATGGTGTGCAGG
CCTGC

121 P D D L S G V I R R L W A D H G V Q A C

421

TTTGGCCGCTCAAGGGAATACCAGCTCAACGACTCAGCTGCCTACTACCTGAACG
ACCTG

141 F G R S R E Y Q L N D S A A Y Y L N D L

481

GAGCGTATTGCACAGAGTGACTACATCCCCACACAGCAAGATGTGCTACGGACCC
GCGTA

161 E R I A Q S D Y I P T Q Q D V L R T R V

541

AAGACCACGGGGATCGTGGAGACACACTTCACCTTCAAGGACCTACACTTCAAGA
TGTTT

181 K T T G I V E T H F T F K D L H F K M F

601

GATGTGGGTGGTCAGCGGTCTGAGCGGAAGAAGTGGATCCACTGCTTTGAGGGCG
TCACA

201 D V G G Q R S E R K K W I H C F E G V T

661

GCCATCATCTTCTGCGTAGCCTTGAGCGCCTATGACTTGGTGCTAGCTGAGGACGA
GGAG

221 A I I F C V A L S A Y D L V L A E D E E

721

ATGAACCGCATGCATGAGAGCATGAAGCTATTCGATAGCATCTGCAACAACAAGT
GGTTC

241 M N R M H E S M K L F D S I C N N K W F

781

ACAGACACGTCCATCATCCTCTTCCTCAACAAGAAGGACCTGTTTGAGGAGAAGA
TCACA

261 T D T S I I L F L N K K D L F E E K I T

841

CACAGTCCCCTGACCATCTGCTTCCCTGAGTACACAGGGGCCAACAAATATGATG
AGGCA

281 H S P L T I C F P E Y T G A N K Y D E A

901

GCCAGCTACATCCAGAGTAAGTTTGAGGACCTGAATAAGCGCAAAGACACCAAGG
AGATC

301 A S Y I Q S K F E D L N K R K D T K E I

961

TACACGCACTTCACGTGCGCCACCGACACCAAGAACGTGCAGTTCGTGTTTGACG
CCGTC

321 Y T H F T C A T D T K N V Q F V F D A V

ClaI

1021

ACCGATGTCATCATCAAGAACAACCTGAAGGACTGCGGCCTCTTCATGCAT

341 T D V I I K N N L K D C G L F

SEQ ID NO.: 196

Human G 12/13

XhoI

1

CTCGAGATGTCCGGGGTGGTGCGGACCCTCAGCCGCTGCCTGCTGCCGGCCGAGG
CCGGCGGGGCC

1 M S G V V R T L S R C L L P A E A G G A

61

CGCGAGCGCAGGGCGGGCAGCGGCGCGCGCGACGCGGAGCGCGAGGCCCGGAGG
CGTAGC

21 R E R R A G S G A R D A E R E A R R R S

121

CGCGACATCGACGCGCTGCTGGCCCGCGAGCGGCGCGCGGTCCGGCGCCTGGTGA
AGATC

41 R D I D A L L A R E R R A V R R L V K I

181

CTGCTGCTGGGCGCGGGCGAGAGCGGCAAGTCCACGTTCCTCAAGCAGATGCGCA
TCATC

61 L L L G A G E S G K S T F L K Q M R I I

241

CACGGCCGCGAGTTCGACCAGAAGGCGCTGCTGGAGTTCCGCGACACCATCTTCG
ACAAC

81 H G R E F D Q K A L L E F R D T I F D N

301

ATCCTCAAGGGCTCAAGGGTTCTTGTTGATGCACGAGATAAGCTTGGCATTCCTTG
GCAG

101 I L K G S R V L V D A R D K L G I P W Q

361

TATTCTGAAAATGAGAAGCATGGGATGTTCCTGATGGCCTTCGAGAACAAGGCGG
GGCTG

121 Y S E N E K H G M F L M A F E N K A G L

421

CCTGTGGAGCCGGCCACCTTCCAGCTGTACGTCCCGGCCCTGAGCGCACTCTGGA
GGGAT

141 P V E P A T F Q L Y V P A L S A L W R D

481

TCTGGCATCAGGGAGGCTTTCAGCCGGAGAAGCGAGTTTCAGCTGGGGGAGTCGG
TGAAG

161 S G I R E A F S R R S E F Q L G E S V K

541

TACTTCCTGGACAACTTGGACCGGATCGGCCAGCTGAATTACTTTCCTAGTAAGCA
AGAT

181 Y F L D N L D R I G Q L N Y F P S K Q D

601

ATCCTGCTGGCTAGGAAAGCCACCAAGGGAATTGTGGAGCATGACTTCGTTATTA
AGAAG

201 I L L A R K A T K G I V E H D F V I K K

661

ATCCCCTTTAAGATGGTGGATGTGGGCGGCCAGCGGTCCCAGCGCCAGAAGTGGT
TCCAG

221 I P F K M V D V G G Q R S Q R Q K W F Q

721

TGCTTCGACGGGATCACGTCCATCCTGTTCATGGTCTCCTCCAGCGAGTACGACCA
GGTC

241 C F D G I T S I L F M V S S S E Y D Q V

781

CTCATGGAGGACAGGCGCACCAACCGGCTGGTGGAGTCCATGAACATCTTCGAGA
CCATC

261 L M E D R R T N R L V E S M N I F E T I

841

GTCAACAACAAGCTCTTCTTCAACGTCTCCATCATTCTCTTCCTCAACAAGATGGA
CCTC

281 V N N K L F F N V S I I L F L N K M D L

901

CTGGTGGAGAAGGTGAAGACCGTGAGCATCAAGAAGCACTTCCCGGACTTCAGGG
GCGAC

301 L V E K V K T V S I K K H F P D F R G D

961

CCGCACCAGCTGGAGGACGTCCAGCGCTACCTGGTCCAGTGCTTCGACAGGAAGA
GACGG

321 P H Q L E D V Q R Y L V Q C F D R K R R

1021

AACCGCAGCAAGCCACTCTTCCACCACTTCACCACCGCCATCGACACCGAGAACG
TCCGC

341 N R S K P L F H H F T T A I D T E N V R

1081

TTCGTGTTCCATGCTGTGAAAGACACCATCCTGCAGGAGAACCTGAAGGACATCA
TGCTG

361 F V F H A V K D T I L Q E N L K D I M L

ClaI

1141 CAGATCGAT

381 Q

SEQ ID NO.: 205

Human 2AR-ToxR (5-141) chimera stop GS1 -ToxR (5-141) chimera transcriptional fusion

SalI +1 B2AR

1 GTCGACATGG GGCAACCCGG GAACGGCAGC GCCTTCTTGC TGGCACCCAA TGGAAGCCAT

61 GCGCCGGACC ACGACGTCAC GCAGCAAAGG GACGAGGTGT GGGTGGTGGG CATGGGCATC

121 GTCATGTCTC TCATCGTCCT GGCCATCGTG TTTGGCAATG TGCTGGTCAT CACAGCCATT

181 GCCAAGTTCG AGCGTCTGCA GACGGTCACC AACTACTTCA TCACTTCACT GGCCTGTGCT

241 GATCTGGTCA TGGGCCTAGC AGTGGTGCCC TTTGGGGCCG CCCATATTCT TATGAAAATG

301 TGGACTTTTG GCAACTTCTG GTGCGAGTTT TGGACTTCCA TTGATGTGCT GTGCGTCACG

361 GCCAGCATTG AGACCCTGTG CGTGATCGCA GTGGATCGCT ACTTTGCCAT TACTTCACCT

421 TTCAAGTACC AGAGCCTGCT GACCAAGAAT AAGGCCCGGG TGATCATTCT GATGGTGTGG

481 ATTGTGTCAG GCCTTAYCTC CTTCTTGCCC ATTCAGATGC ACTGGTACAG GGCCACCCAC

541 CAGGAAGCCA TCAACTGCTA TGCCAATGAG ACCTGCTGTG ACTTCTTCAC GAACCAAGCC

601 TATGCCATTG CCTCTTCCAT CGTGTCCTTC TACGTTCCCC TGGTGATCAT GGTCTTCGTC

661 TACTCCAGGG TCTTTCAGGA GGCCAAAAGG CAGCTCCAGA AGATTGACAA ATCTGAGGGC

721 CGCTTCCATG TCCAGAACCT TAGCCAGGTG GAGCAGGATG GGCGGACGGG GCATGGACTC

781 CGCAGATCTT CCAAGTTCTG CTTGAAGGAG CACAAAGCCC TCAAGACGTT AGGCATCATC

841 ATGGGCACTT TCACCCTCTG CTGGCTGCCC TTCTTCATCG TTAACATTGT GCATGTGATC

901 CAGGATAACC TCATCCGTAA GGAAGTTTAC ATCCTCCTAA ATTGGATAGG CTATGTCAAT

961 TCTGGTTTCA ATCCCCTTAT CTACTGCCGG AGCCCAGATT TCAGGATTGC CTTCCAGGAG

1021 CTTCTGTGCC TGCGCAGGTC TTCTTTGAAG GCCTATGGCA ATGGCTACTC CAGCAACGGC

1081 AACACAGGGG AGCAGAGTGG ATATCACGTG GAACAGGAGA AAGAAAATAA ACTGCTGTGT

1141 GAAGACCTCC CAGGCACGGA AGACTTTGTG GGCCATCAAG GTACTGTGCC TAGCGATAAC

last B2AR linker sequence

1201 ATTGATTCAC AAGGGAGGAA TTGTAGTACA AATGACTCAC TGCTAGAGCG TGGCCAGACG

PstI +5 toxR (5-141)

1261 GTCACCAACC TGCAGGGACA CAACTCAAAA GAGATATCGA TGAGTCATAT TGGTACTAAA

1321 TTCATTCTTG CTGAAAAATT TACCTTCGAT CCCCTAAGCA ATACTCTGAT TGACAAAGAA

1381 GATAGTGAAG AGATCATTCG ATTAGGCAGC AACGAAAGCC GAATTCTTTG GCTGCTGGCC

1441 CAACGTCCAA ACGAGGTAAT TTCTCGCAAT GATTTGCATG ACTTTGTTTG GCGAGAGCAA

1501 GGTTTTGAAG TCGATGATTC CAGCTTAACC CAAGCCATTT CGACTCTGCG CAAAATGCTC

1561 AAAGATTCGA CAAAGTCCCC ACAATACGTC AAAACGGTTC CGAAGCGCGG TTACCAATTG

1621 ATCGCCCGAG TGGAAACGGT TGAAGAAGAG ATGGCTCGCG AAAACGAAGC TGCTCATGAC

stop SD XhoI +1 GS1 alpha

1681 ATCTCTTAAT AATCAAGGAG GCCCTCGAGA TGGGCTGCCT CGGGAACAGT AAGACCGAGG

1741 ACCAGCGCAA CGAGGAGAAG GCGCAGCGTG AGGCCAACAA AAAGATCGAG AAGCAGCTGC

1801 AGAAGGACAA GCAGGTCTAC CGGGCCACGC ACCGCCTGCT GCTGCTGGGT GCTGGAGAAT

1861 CTGGTAAAAG CACCATTGTG AAGCAGATGA GGATCCTGCA TGTTAATGGG TTTAATGGAG

1921 ACAGTGAGAA GGCAACCAAA GTGCAGGACA TCAAAAACAA CCTGAAAGAG GCGATTGAAA

1981 CCATTGTGGC CGCCATGAGC AACCTGGTGC CCCCCGTGGA GCTGGCCAAC CCCGAGAACC

2041 AGTTCAGAGT GGACTACATC CTGAGTGTGA TGAACGTGCC TGACTTTGAC TTCCCTCCCG

2101 AATTCTATGA GCATGCCAAG GCTCTGTGGG AGGATGAAGG AGTGCGTGCC TGCTACGAAC

2161 GCTCCAACGA GTACCAGCTG ATTGACTGTG CCCAGTACTT CCTGGACAAG ATCGACGTGA

2221 TCAAGCAGGC TGACTATGTG CCGAGCGATC AGGACCTGCT TCGCTGCCGT GTCCTGACTT

2281 CTGGAATCTT TGAGACCAAG TTCCAGGTGG ACAAAGTCAA CTTCCACATG TTTGACGTGG

2341 GTGGCCAGCG CGATGAACGC CGCAAGTGGA TCCAGTGCTT CAACGATGTG ACTGCCATCA

2401 TCTTCGTGGT GGCCAGCAGC AGCTACAACA TGGTCATCCG GGAGGACAAC CAGACCAACC

2461 GCCTGCAGGA GGCTCTGAAC CTCTTCAAGA GCATCTGGAA CAACAGATGG CTGCGCACCA

2521 TCTCTGTGAT CCTGTTCCTC AACAAGCAAG ATCTGCTCGC TGAGAAAGTC CTTGCTGGGA

2581 AATCGAAGAT TGAGGACTAC TTTCCAGAAT TTGCTCGCTA CACTACTCCT GAGGATGCTA

2641 CTCCCGAGCC CGGAGAGGAC CCACGCGTGA CCCGGGCCAA GTACTTCATT CGAGATGAGT

2701 TTCTGAGGAT CAGCACTGCC AGTGGAGATG GGCGTCACTA CTGCTACCCT CATTTCACCT

2761 GCGCTGTGGA CACTGAGAAC ATCCGCCGTG TGTTCAACGA CTGCCGTGAC ATCATTCAGC

ClaI +5 toxR (5-141)

2821 GCATGCACCT TCGTCAGTAC GAGCTGCTCA TCGATGGACA CAACTCAAAA GAGATATCGA

2881 TGAGTCATAT TGGTACTAAA TTCATTCTTG CTGAAAAATT TACCTTCGAT CCCCTAAGCA

2941 ATACTCTGAT TGACAAAGAA GATAGTGAAG AGATCATTCG ATTAGGCAGC AACGAAAGCC

3001 GAATTCTTTG GCTGCTGGCC CAACGTCCAA ACGAGGTAAT TTCTCGCAAT GATTTGCATG

3061 ACTTTGTTTG GCGAGAGCAA GGTTTTGAAG TCGATGATTC CAGCTTAACC CAAGCCATTT

3121 CGACTCTGCG CAAAATGCTC AAAGATTCGA CAAAGTCCCC ACAATACGTC AAAACGGTTC

3181 CGAAGCGCGG TTACCAATTG ATCGCCCGAG TGGAAACGGT TGAAGAAGAG ATGGCTCGCG

Stop XbaI

Stem-loop

3241 AAAACGAAGC TGCTCATGAC ATCTCTTAAT AATCTAGAGG ATCCCCGCGC CCTCATCCGA

3301 AAGGGCG

SEQ ID NO.: 208

Vibrio cholerae Pctx::lacZ reporter fusion constuct

XbaI

1 TCTAGAGGCT GTGGGTAGAA GTGAAACGGG GTTTACCGAT AAAAACAGAA AATGATAAAA

3 ToxR binding repeats

61 AAGGACTAAA TAGTATATTT TGATTTTTGA TTTTTGATTT CAAATAATAC AAATTTATTT

+1 lacZ

121 ACTTATTTAA TTGTTTTGAT CAATTATTTT TCTGTTAAAC AAAGGGAGCA TTATATGGTA

181 AAGACCATGA TTACGGATTC ACTGGCCGTC GTTTTACAAC GTCGTGACTG GGAAAACCCT

241 GGCGTTACCC AACTTAATCG CCTTGCAGCA CATCCCCCTT TCGCCAGCTG GCGTAATAGC

301 GAAGAGGCCC GCACCGATCG CCCTTCCCAA CAGTTGCGCA GCCTGAATGG CGAATGGCGC

361 TTTGCCTGGT TTCCGGCACC AGAAGCGGTG CCGGAAAGCT GGCTGGAGTG CGATCTTCCT

421 GAGGCCGATA CTGTCGTCGT CCCCTCAAAC TGGCAGATGC ACGGTTACGA TGCGCCCATC

481 TACACCAACG TGACCTATCC CATTACGGTC AATCCGCCGT TTGTTCCCAC GGAGAATCCG

541 ACGGGTTGTT ACTCGCTCAC ATTTAATGTT GATGAAAGCT GGCTACAGGA AGGCCAGACG

601 CGAATTATTT TTGATGGCGT TAACTCGGCG TTTCATCTGT GGTGCAACGG GCGCTGGGTC

661 GGTTACGGCC AGGACAGTCG TTTGCCGTCT GAATTTGACC TGAGCGCATT TTTACGCGCC

721 GGAGAAAACC GCCTCGCGGT GATGGTGCTG CGCTGGAGTG ACGGCAGTTA TCTGGAAGAT

781 CAGGATATGT GGCGGATGAG CGGCATTTTC CGTGACGTCT CGTTGCTGCA TAAACCGACT

841 ACACAAATCA GCGATTTCCA TGTTGCCACT CGCTTTAATG ATGATTTCAG CCGCGCTGTA

901 CTGGAGGCTG AAGTTCAGAT GTGCGGCGAG TTGCGTGACT ACCTACGGGT AACAGTTTCT

961 TTATGGCAGG GTGAAACGCA GGTCGCCAGC GGCACCGCGC CTTTCGGCGG TGAAATTATC

1021 GATGAGCGTG GTGGTTATGC CGATCGCGTC ACACTACGTC TGAACGTCGA AAACCCGAAA

1081 CTGTGGAGCG CCGAAATCCC GAATCTCTAT CGTGCGGTGG TTGAACTGCA CACCGCCGAC

1141 GGCACGCTGA TTGAAGCAGA AGCCTGCGAT GTCGGTTTCC GCGAGGTGCG GATTGAAAAT

1201 GGTCTGCTGC TGCTGAACGG CAAGCCGTTG CTGATTCGAG GCGTTAACCG TCACGAGCAT

1261 CATCCTCTGC ATGGTCAGGT CATGGATGAG CAGACGATGG TGCAGGATAT CCTGCTGATG

1321 AAGCAGAACA ACTTTAACGC CGTGCGCTGT TCGCATTATC CGAACCATCC GCTGTGGTAC

1381 ACGCTGTGCG ACCGCTACGG CCTGTATGTG GTGGATGAAG CCAATATTGA AACCCACGGC

1441 ATGGTGCCAA TGAATCGTCT GACCGATGAT CCGCGCTGGC TACCGGCGAT GAGCGAACGC

1501 GTAACGCGAA TGGTGCAGCG CGATCGTAAT CACCCGAGTG TGATCATCTG GTCGCTGGGG

1561 AATGAATCAG GCCACGGCGC TAATCACGAC GCGCTGTATC GCTGGATCAA ATCTGTCGAT

1621 CCTTCCCGCC CGGTGCAGTA TGAAGGCGGC GGAGCCGACA CCACGGCCAC CGATATTATT

1681 TGCCCGATGT ACGCGCGCGT GGATGAAGAC CAGCCCTTCC CGGCTGTGCC GAAATGGTCC

1741 ATCAAAAAAT GGCTTTCGCT ACCTGGAGAG ACGCGCCCGC TGATCCTTTG CGAATACGCC

1801 CACGCGATGG GTAACAGTCT TGGCGGTTTC GCTAAATACT GGCAGGCGTT TCGTCAGTAT

1861 CCCCGTTTAC AGGGCGGCTT CGTCTGGGAC TGGGTGGATC AGTCGCTGAT TAAATATGAT

1921 GAAAACGGCA ACCCGTGGTC GGCTTACGGC GGTGATTTTG GCGATACGCC GAACGATCGC

1981 CAGTTCTGTA TGAACGGTCT GGTCTTTGCC GACCGCACGC CGCATCCAGC GCTGACGGAA

2041 GCAAAACACC AGCAGCAGTT TTTCCAGTTC CGTTTATCCG GGCAAACCAT CGAAGTGACC

2101 AGCGAATACC TGTTCCGTCA TAGCGATAAC GAGCTCCTGC ACTGGATGGT GGCGCTGGAT

2161 GGTAAGCCGC TGGCAAGCGG TGAAGTGCCT CTGGATGTCG CTCCACAAGG TAAACAGTTG

2221 ATTGAACTGC CTGAACTACC GCAGCCGGAG AGCGCCGGGC AACTCTGGCT CACAGTACGC

2281 GTAGTGCAAC CGAACGCGAC CGCATGGTCA GAAGCCGGGC ACATCAGCGC CTGGCAGCAG

2341 TGGCGTCTGG CGGAAAACCT CAGTGTGACG CTCCCCGCCG CGTCCCACGC CATCCCGCAT

2401 CTGACCACCA GCGAAATGGA TTTTTGCATC GAGCTGGGTA ATAAGCGTTG GCAATTTAAC

2461 CGCCAGTCAG GCTTTCTTTC ACAGATGTGG ATTGGCGATA AAAAACAACT GCTGACGCCG

2521 CTGCGCGATC AGTTCACCCG TGCACCGCTG GATAACGACA TTGGCGTAAG TGAAGCGACC

2581 CGCATTGACC CTAACGCCTG GGTCGAACGC TGGAAGGCGG CGGGCCATTA CCAGGCCGAA

2641 GCAGCGTTGT TGCAGTGCAC GGCAGATACA CTTGCTGATG CGGTGCTGAT TACGACCGCT

2701 CACGCGTGGC AGCATCAGGG GAAAACCTTA TTTATCAGCC GGAAAACCTA CCGGATTGAT

2761 GGTAGTGGTC AAATGGCGAT TACCGTTGAT GTTGAAGTGG CGAGCGATAC ACCGCATCCG

2821 GCGCGGATTG GCCTGAACTG CCAGCTGGCG CAGGTAGCAG AGCGGGTAAA CTGGCTCGGA

2881 TTAGGGCCGC AAGAAAACTA TCCCGACCGC CTTACTGCCG CCTGTTTTGA CCGCTGGGAT

2941 CTGCCATTGT CAGACATGTA TACCCCGTAC GTCTTCCCGA GCGAAAACGG TCTGCGCTGC

3001 GGGACGCGCG AATTGAATTA TGGCCCACAC CAGTGGCGCG GCGACTTCCA GTTCAACATC

3061 AGCCGCTACA GTCAACAGCA ACTGATGGAA ACCAGCCATC GCCATCTGCT GCACGCGGAA

3121 GAAGGCACAT GGCTGAATAT CGACGGTTTC CATATGGGGA TTGGTGGCGA CGACTCCTGG

3181 AGCCCGTCAG TATCGGCGGA ATTCCAGCTG AGCGCCGGTC GCTACCATTA CCAGTTGGTC

Stop Stem-loop XbaI

3241 TGGTGTCAAA AATAATAACGCCCTCAT CCGAAAGGGC GTCTAGA

SEQ ID NO.: 266

pMPX-74 MalE (1-28) fusion vector

SD old PstI +1

2401

GAATTCAGGCGCTTTTTAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCATATGA
AAAT

1 M K I

2461

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCC
GCCTC

4 K T G A R I L A L S A L T T M M F S A S

Factor Xa PstI SalI XbaI

2521

GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCT
AGAGA

24 A L A K I I E A R L Q A S V D A E S R D

FLAG lost XbaI

2581 TTATAAAGATGACGATGACAAATAATAAGCTAGAGG

(transcriptional stop)

44 Y K D D D D K

pMPX-72::malE(1-28)::FXa::PstI, SalI, XbaI::FLAG

Rhamnose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-72 cut with PstI & XbaI.

SEQ ID NO.: 267

pMPX-75 MalE (1-28) fusion vector

SD old PstI +1

1621

CCATACCCGTTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAAACAGG

TGCAC

1 M K I K T G A

1681

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC
AAAA

8 R I L A L S A L T T M M F S A S A L A K

Factor Xa PstI SalI XbaI
FLAG

1741

TCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCTAGAGATTATAAAGA
TGACG

Lost XbaI

1801 ATGACAAATAATAAGCTAGAGG (Transcriptional stop)

pMPX-71::malE(1-28)::FXa::PstI, SalI, XbaI::FLAG

Arabinose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-71 cut with PstI & XbaI.

SEQ ID NO.: 268

pMPX-88 MalE (1-28) fusion vector

SD old PstI +1

AGGAGGTTCTGCATATGAAAAT

1 M K I

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCC
GCCTC

4 K T G A R I L A L S A L T T M M F S A S

Factor Xa PstI SalI XbaI

GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCT
AGAGA

24 A L A K I I E A R L Q A S V D A E S R D

FLAG lost XbaI

TTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC
(transcriptional stop)

44 Y K D D D D K

pMPX-84::malE(1-28)::FXa::PstI, SalI, XbaI::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-84 cut with PstI & XbaI.

SEQ ID NO.: 269

pMPX-93 MalE (1-28) fusion vector

SD old PstI +1

AGGAGGTTCTGCATATGAAAAT

1 M K I

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCC
GCCTC

4 K T G A R I L A L S A L T T M M F S A S

5

Factor Xa PstI SalI XbaI

GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCT
AGAGA

10 24 A L A K I I E A R L Q A S V D A E S R D

FLAG lost XbaI

TTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC
(transcriptional stop)

15 44 Y K D D D D K

pMPX-86::malE(1-28)::FXa::PstI, SalI, XbaI::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

20 Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-86 cut with PstI & XbaI.

SEQ ID NO.: 270

pMPX-77 MalE (1-370 del 354-364) fusion vector

SD old PstI +1

2401

GAATTCAGGCGCTTTTTAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCATATGA
AAAT

1 M K I

2461

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCC
GCCTC

4 K T G A R I L A L S A L T T M M F S A S

2521

GGCTCTCGCCAAAATCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAA
GGCTA

24 A L A K I E E G K L V I W I N G D K G Y

2581

TAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTC
ACCGT

44 N G L A E V G K K F E K D T G I K V T V

2641

TGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGAT
GGCCC

64 E H P D K L E E K F P Q V A A T G D G P

2701

TGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGT
TGGC

84 D I I F W A H D R F G G Y A Q S G L L A

2761

TGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGAT
GCCGT

104 E I T P D K A F Q D K L Y P F T W D A V

2821

ACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGA
TTTA

124 R Y N G K L I A Y P I A V E A L S L I Y

2881

TAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTG
GATAA

144 N K D L L P N P P K T W E E I P A L D K

2941

AGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTAC
TTCAC

164 E L K A K G K S A L M F N L Q E P Y F T

3001

CTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAG
TACGA

184 W P L I A A D G G Y A F K Y E N G K Y D

3061

CATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTG
GTTGA

204 I K D V G V D N A G A K A G L T F L V D

3121

CCTGATTAAAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCT
GCCTT

224 L I K N K H M N A D T D Y S I A E A A F

3181

TAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATC
GACAC

244 N K G E T A M T I N G P W A W S N I D T

3241

CAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCC
AAACC

264 S K V N Y G V T V L P T F K G Q P S K P

3301

GTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTG
GCGAA

284 F V G V L S A G I N A A S P N K E L A K

3361

AGAGTTCCTCGAAAACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAA
GACAA

304 E F L E N Y L L T D E G L E A V N K D K

3421

ACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCA
CGTAT

324 P L G A V A L K S Y E E E L A K D P R I

pMPX-72::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG

Rhamnose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-72 cut with PstI & XbaI.

SEQ ID NO.: 271

pMPX-76 MalE (1-370 del 354-364) fusion vector

SD old PstI +1

1621
CCATACCCGTTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAAACAGG
TGCAC

1 M K I K T G A

1681
GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC
AAAA

8 R I L A L S A L T T M M F S A S A L A K

1741
TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCT
CGCTG

28 I E E G K L V I W I N G D K G Y N G L A

1801
AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCC
GGATA

48 E V G K K F E K D T G I K V T V E H P D

1861
AACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTAT
CTTCT

68 K L E E K F P Q V A A T G D G P D I I F

1921
GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCAC
CCCGG

88 W A H D R F G G Y A Q S G L L A E I T P

1981
ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAA
CGGCA

108 D K A F Q D K L Y P F T W D A V R Y N G

2041
AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGAT
CTGC

128 K L I A Y P I A V E A L S L I Y N K D L

2101
TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGA
AAGCGA

148 L P N P P K T W E E I P A L D K E L K A

2161
AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCT
GATTG

168 K G K S A L M F N L Q E P Y F T W P L I

2221
CTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGA
CGTGG

188 A A D G G Y A F K Y E N G K Y D I K D V

2281
GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAA
AAACA

208 G V D N A G A K A G L T F L V D L I K N

2341
AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGG
CGAAA

228 K H M N A D T D Y S I A E A A F N K G E

2401
CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGT
GAATT

248 T A M T I N G P W A W S N I D T S K V N

2461

ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGG
CGTGC

268 Y G V T V L P T F K G Q P S K P F V G V

2521

TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCT
CGAAA

288 L S A G I N A A S P N K E L A K E F L E

2581

ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGG
TGCCG

308 N Y L L T D E G L E A V N K D K P L G A

2641

TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCAC
CATGG

328 V A L K S Y E E E L A K D P R I A A T M

Factor Xa PstI

2701

AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGC
CTCGG

348 E N A Q S A F W Y A V R I E A R L Q A S

SalI XbaI FLAG Lost XbaI

2761

TCGACGCCGAATCTAGAGATTATAAAGATGACGATGACAAATAATAAGCTAGAGG
A(trxn stop)

368 V D A E S R D Y K D D D D K

pMPX-71::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG

Arabinose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-71 cut with PstI & XbaI.

SEQ ID NO.: 272

pMPX-89 MalE (1-370 del 354-364) fusion vector

SD old PstI +1

AGGAGGTTCTGCATATGAAAATAAAAACAGGTGCAC

1 M K I K T G A

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC
AAAA

8 R I L A L S A L T T M M F S A S A L A K

TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCT
CGCTG

28 I E E G K L V I W I N G D K G Y N G L A

AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCC
GGATA

48 E V G K K F E K D T G I K V T V E H P D

AACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTAT
CTTCT

68 K L E E K F P Q V A A T G D G P D I I F

GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCAC
CCCGG

88 W A H D R F G G Y A Q S G L L A E I T P

ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAA
CGGCA

108 D K A F Q D K L Y P F T W D A V R Y N G

AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGAT
CTGC

128 K L I A Y P I A V E A L S L I Y N K D L

TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGA
AAGCGA

148 L P N P P K T W E E I P A L D K E L K A

AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCT
GATTG

168 K G K S A L M F N L Q E P Y F T W P L I

CTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGA
CGTGG

188 A A D G G Y A F K Y E N G K Y D I K D V

GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAA
AAACA

208 G V D N A G A K A G L T F L V D L I K N

AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGG
CGAAA

228 K H M N A D T D Y S I A E A A F N K G E

CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGT
GAATT

248 T A M T I N G P W A W S N I D T S K V N

ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGG
CGTGC

268 Y G V T V L P T F K G Q P S K P F V G V

TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCT
CGAAA

288 L S A G I N A A S P N K E L A K E F L E

ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGG
TGCCG

308 N Y L L T D E G L E A V N K D K P L G A

TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCAC
CATGG

328 V A L K S Y E E E L A K D P R I A A T M

Factor Xa PstI

AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGC
CTCGG

348 E N A Q S A F W Y A V R I E A R L Q A S

SalI XbaI FLAG Lost XbaI

TCGACGCCGAATCTAGAGATTATAAAGATGACGATGACAAATAATAAGCTAGAGG
(trxn stop)

368 V D A E S R D Y K D D D D K

pMPX-84::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-84 cut with PstI & XbaI.

SEQ ID NO.: 273

pMPX-94 MalE (1-370 del 354-364) fusion vector

SD old PstI +1

AGGAGGTTCTGCATATGAAAATAAAAACAGGTGCAC

1 M K I K T G A

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC
AAAA

8 R I L A L S A L T T M M F S A S A L A K

TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCT
CGCTG

28 I E E G K L V I W I N G D K G Y N G L A

AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCC
GGATA

48 E V G K K F E K D T G I K V T V E H P D

AACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTAT
CTTCT

68 K L E E K F P Q V A A T G D G P D I I F

GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCAC
CCCGG

88 W A H D R F G G Y A Q S G L L A E I T P

ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAA
CGGCA

108 D K A F Q D K L Y P F T W D A V R Y N G

AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGAT
CTGC

128 K L I A Y P I A V E A L S L I Y N K D L

TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGA
AAGCGA

148 L P N P P K T W E E I P A L D K E L K A

AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCT
GATTG

168 K G K S A L M F N L Q E P Y F T W P L I

CTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGA
CGTGG

188 A A D G G Y A F K Y E N G K Y D I K D V

GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAA
AAACA

208 G V D N A G A K A G L T F L V D L I K N

AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGG
CGAAA

228 K H M N A D T D Y S I A E A A F N K G E

CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGT
GAATT

248 T A M T I N G P W A W S N I D T S K V N

ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGG
CGTGC

268 Y G V T V L P T F K G Q P S K P F V G V

TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCT
CGAAA

288 L S A G I N A A S P N K E L A K E F L E

ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGG
TGCCG

308 N Y L L T D E G L E A V N K D K P L G A

TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCAC
CATGG

328 V A L K S Y E E E L A K D P R I A A T M

Factor Xa PstI

AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGC
CTCGG

348 E N A Q S A F W Y A V R I E A R L Q A S

SalI XbaI FLAG Lost XbaI

TCGACGCCGAATCTAGAGATTATAAAGATGACGATGACAAATAATAAGCTAGAGG
(trxn stop)

368 V D A E S R D Y K D D D D K

pMPX-86::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-86 cut with PstI & XbaI.

SEQ ID NO.: 274

pMPX-79 TrxA (2-109 del 103-107) fusion vector

SD PstI SalI XbaI +2 trxA(del 103-107)

1
TAGCAGGAGGCCCTGCAGGCCTCGGTCGACGCCGAATCTAGAAGCGATAAAATTATT

1 A S V D A E S R S D K I I

61
CACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTC

17 H L T D D S F D T D V L K A D G A I L V

121
GATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGAAATC

37 D F W A E W C G P C K M I A P I L D E I

181
GCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAACATCGATCAAAACCCTGGC

57 A D E Y Q G K L T V A K L N I D Q N P G

241

ACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACG
GTGAA

77 T A P K Y G I R G I P T L L L F K N G E

301

GTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGG
CGGAT

97 V A A T K V G A L S K G Q L K E N L A D

FLAG Lost XbaI

361 TATAAAGATGACGATGACAAATAATAAGCTAGAGG (transcriptional stop)

117 Y K D D D D K

pMPX-71::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG

Arabinose inducible, clone into PstI, SalI, XbaI

+1 Met required for protein to be fused

Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-NheI insertion with PstI & NheI and cloning into pMPX-71 cut with PstI & XbaI.

SEQ ID NO.: 275

pMPX-78 TrxA (2-109 del 103-107) fusion vector

SD PstI

1
GAATTCAGGCGCTTTTTAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCAGGCCT
C

1 A S

SalI XbaI +2 trxA(del 103-107)

61
GGTCGACGCCGAATCTAGAAGCGATAAAATTATTCACCTGACTGACGACAGTTTT
GACAC

6 V D A E S R S D K I I H L T D D S F D T

121
GGATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGC
GGTCC

26 D V L K A D G A I L V D F W A E W C G P

181

GTGCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAA
CTGAC

46 C K M I A P I L D E I A D E Y Q G K L T

241

CGTTGCAAAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATC
CGTGG

66 V A K L N I D Q N P G T A P K Y G I R G

301

TATCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGT
GCACT

86 I P T L L L F K N G E V A A T K V G A L

FLAG

361

GTCTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAA
TAATAA

106 S K G Q L K E N L A D Y K D D D D K

lost XbaI

GCTAGAGG (transcriptional stop)

pMPX-72::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG

Rhamnose inducible, clone into PstI, SalI, XbaI

+1 Met required for protein to be fused

Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-NheI insertion with PstI & NheI and cloning into pMPX-72 cut with PstI & XbaI.

SEQ ID NO.: 276

pMPX-90 TrxA (2-109 del 103-107) fusion vector

SD PstI SalI XbaI +2 trxA(del 103-107)

AGGAGGTTCTGCAGGCCTCGGTCGACGCCGAATCTAGAAGCGATAAAATTATT

1 A S V D A E S R S D K I I

CACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCC TCGTC

17 H L T D D S F D T D V L K A D G A I L V

GATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATG
AAATC

37 D F W A E W C G P C K M I A P I L D E I

GCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAACATCGATCAAAACC
CTGGC

57 A D E Y Q G K L T V A K L N I D Q N P G

ACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACG
GTGAA

77 T A P K Y G I R G I P T L L L F K N G E

GTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGG
CGGAT

97 V A A T K V G A L S K G Q L K E N L A D

FLAG Lost XbaI

TATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC
(transcriptional stop)

117 Y K D D D D K

pMPX-84::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

+1 Met required for protein to be fused

Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-NheI insertion with PstI & NheI and cloning into pMPX-84 cut with PstI & XbaI.

SEQ ID NO.: 277

pMPX-95 TrxA (2-109 del 103-107) fusion vector

SD PstI SalI XbaI +2 trxA(del 103-107)

AGGAGGTTCTGCAGGCCTCGGTCGACGCCGAATCTAGAAGCGATAAAATTATT

1 A S V D A E S R S D K I I

CACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCC
TCGTC

17 H L T D D S F D T D V L K A D G A I L V

GATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATG
AAATC

37 D F W A E W C G P C K M I A P I L D E I

GCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAACATCGATCAAAACC
CTGGC

57 A D E Y Q G K L T V A K L N I D Q N P G

ACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACG
GTGAA

77 T A P K Y G I R G I P T L L L F K N G E

GTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGG
CGGAT

97 V A A T K V G A L S K G Q L K E N L A D

FLAG Lost XbaI

TATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC
(transcriptional stop)

117 Y K D D D D K

pMPX-86::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG

Temperature inducible, clone into PstI, SalI, XbaI.

+1 Met required for protein to be fused

Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-NheI insertion with PstI & NheI and cloning into pMPX-86 cut with PstI & XbaI.

SEQ ID NO.: 278

pMPX-80 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1

malE(1-28)

2401

GAATTCAGGCGCTTTTTAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCATATGA
AAAT

1 M K I

2461

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCC
GCCTC

4 K T G A R I L A L S A L T T M M F S A S

Factor Xa PstI SalI XbaI

2521

GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCT
AGAAG

24 A L A K I I E A R L Q A S V D A E S R S

+2 trxA (2-109 del 103-107)

2581

CGATAAAATTATTCACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCG
GACGG

44 D K I I H L T D D S F D T D V L K A D G

2641

GGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCC
CCGAT

64 A I L V D F W A E W C G P C K M I A P I

2701

TCTGGATGAAATCGCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAAC
ATCGA

84 L D E I A D E Y Q G K L T V A K L N I D

2761

TCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTG
CTGTT

104 Q N P G T A P K Y G I R G I P T L L L F

2821

CAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTG
AAAGA

124 K N G E V A A T K V G A L S K G Q L K E

FLAG Lost XbaI

2881

GAACCTGGCGGATTATAAAGATGACGATGACAAATAATAAGCTAGAGG (trxn stop)

144 N L A D Y K D D D D K

pMPX-72::malE(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

Rhamnose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-78 cut with PstI & XbaI.

SEQ ID NO.: 279

pMPX-81 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1 malE (1-28)

1621

CCATACCCGTTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAAACAGG
TGCAC

1 M K I K T G A

1681

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC
AAAA

8 R I L A L S A L T T M M F S A S A L A K

+2 trxA(2-109 del 103-107) Factor Xa PstI SalI XbaI

1741

TCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCTAGAAGCGATAAAAT
TATTC

28 I I E A R L Q A S V D A E S R S D K I I

1801

ACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCT
CGTCG

48 H L T D D S F D T D V L K A D G A I L V

1861

ATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGA
AATCG

68 D F W A E W C G P C K M I A P I L D E I

1921
CTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAACATCGATCAAAACCC
TGGCA

88 A D E Y Q G K L T V A K L N I D Q N P G

1981
CTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACGGT
GAAG

108 T A P K Y G I R G I P T L L L F K N G E

2041
TGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGGC
GGATT

128 V A A T K V G A L S K G Q L K E N L A D

FLAG

2101 ATAAAGATGACGATGACAAATAATAAGCTAGAGG (transcriptional stop)

148 Y K D D D D K

pMPX-71::malE(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

Arabinose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-79 cut with PstI & XbaI.

SEQ ID NO.: 280

pMPX-91 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1

malE(1-28)

AGGAGGTTCTGCATATGAAAAT

1 M K I

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCC GCCTC

4 K T G A R I L A L S A L T T M M F S A S

Factor Xa PstI SalI XbaI

GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCT AGAAG

24 A L A K I I E A R L Q A S V D A E S R S

+2 trxA (2-109 del 103-107)

CGATAAAATTATTCACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCG
GACGG

44 D K I I H L T D D S F D T D V L K A D G

GGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCC
CCGAT

64 A I L V D F W A E W C G P C K M I A P I

TCTGGATGAAATCGCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAAC
ATCGA

84 L D E I A D E Y Q G K L T V A K L N I D

TCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTG
CTGTT

104 Q N P G T A P K Y G I R G I P T L L L F

CAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTG
AAAGA

124 K N G E V A A T K V G A L S K G Q L K E

FLAG Lost XbaI

GAACCTGGCGGATTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC

(trxn stop)

144 N L A D Y K D D D D K

pMPX-84::malE(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-90 cut with PstI & XbaI.

SEQ ID NO.: 281

pMPX-96 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1

malE(1-28)

AGGAGGTTCTGCATATGAAAAT

1 M K I

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCC
5 GCCTC

4 K T G A R I L A L S A L T T M M F S A S

Factor Xa PstI SalI XbaI

10 GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCT
AGAAG

24 A L A K I I E A R L Q A S V D A E S R S

+2 trxA (2-109 del 103-107)

15

CGATAAAATTATTCACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCG
GACGG

44 D K I I H L T D D S F D T D V L K A D G

20

GGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCC
CCGAT

64 A I L V D F W A E W C G P C K M I A P I

TCTGGATGAAATCGCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAAC
ATCGA

84 L D E I A D E Y Q G K L T V A K L N I D

TCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTG
CTGTT

104 Q N P G T A P K Y G I R G I P T L L L F

CAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTG
AAAGA

124 K N G E V A A T K V G A L S K G Q L K E

FLAG Lost XbaI

GAACCTGGCGGATTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC
(trxn stop)

144 N L A D Y K D D D D K

pMPX-86::malE(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-95 cut with PstI & XbaI.

SEQ ID NO.: 282

pMPX-83 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1

malE(1-28)

2401

GAATTCAGGCGCTTTTTAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCATATGAAAAT

1 M K I

2461

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTC

4 K T G A R I L A L S A L T T M M F S A S

2521

GGCTCTCGCCAAAATCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTA

24 A L A K I E E G K L V I W I N G D K G Y

2581
TAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTC
ACCGT

44 N G L A E V G K K F E K D T G I K V T V

2641
TGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGAT
GGCCC

64 E H P D K L E E K F P Q V A A T G D G P

2701
TGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGT
TGGC

84 D I I F W A H D R F G G Y A Q S G L L A

2761
TGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGAT
GCCGT

104 E I T P D K A F Q D K L Y P F T W D A V

2821
ACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGA
TTTA

124 R Y N G K L I A Y P I A V E A L S L I Y

2881

TAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTG
GATAA

144 N K D L L P N P P K T W E E I P A L D K

2941

AGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTAC
TTCAC

164 E L K A K G K S A L M F N L Q E P Y F T

3001

CTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAG
TACGA

184 W P L I A A D G G Y A F K Y E N G K Y D

3061

CATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTG
GTTGA

204 I K D V G V D N A G A K A G L T F L V D

3121

CCTGATTAAAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCT
GCCTT

224 L I K N K H M N A D T D Y S I A E A A F

3181
TAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATC
GACAC

244 N K G E T A M T I N G P W A W S N I D T

3241
CAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCC
AAACC

264 S K V N Y G V T V L P T F K G Q P S K P

3301
GTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTG
GCGAA

284 F V G V L S A G I N A A S P N K E L A K

3361
AGAGTTCCTCGAAAACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAA
GACAA

304 E F L E N Y L L T D E G L E A V N K D K

3421
ACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCA
CGTAT

324 P L G A V A L K S Y E E E L A K D P R I

Factor Xa

3481

TGCCGCCACCATGGAAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAA
GCCCG

344 A A T M E N A Q S A F W Y A V R I E A R

PstI SalI XbaI +2 trxA (2-109 del 103-107)

3541

CCTGCAGGCCTCGGTCGACGCCGAATCTAGAAGCGATAAAATTATTCACCTGACT
GACGA

364 L Q A S V D A E S R S D K I I H L T D D

3601

CAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGG
GCAGA

384 S F D T D V L K A D G A I L V D F W A E

3661

GTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAA
TATCA

404 W C G P C K M I A P I L D E I A D E Y Q

3721

GGGCAAACTGACCGTTGCAAAACTGAACATCGATCAAAACCCTGGCACTGCGCCG
AAATA

424 G K L T V A K L N I D Q N P G T A P K Y

3781
TGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCA
ACCAA

444 G I R G I P T L L L F K N G E V A A T K

FLAG

3841
AGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGAT
GACGA

464 V G A L S K G Q L K E N L A D Y K D D D

3901 TGACAAATAATAAGCTAGAGG (transcriptional stop)

484 D K

pMPX-72::malE(1-320 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG.

Rhamnose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-78 cut with PstI & XbaI.

SEQ ID NO.: 283

pMPX-82 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1 malE (1-370 del 352-362)

1621
CCATACCCGTTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAAACAGG
TGCAC

1 M K I K T G A

1681
GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC
AAAA

8 R I L A L S A L T T M M F S A S A L A K

1741
TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCT
CGCTG

28 I E E G K L V I W I N G D K G Y N G L A

1801
AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCC
GGATA

48 E V G K K F E K D T G I K V T V E H P D

1861
AACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTAT
CTTCT

68 K L E E K F P Q V A A T G D G P D I I F

1921
GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCAC
CCCGG

88 W A H D R F G G Y A Q S G L L A E I T P

1981
ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAA
CGGCA

108 D K A F Q D K L Y P F T W D A V R Y N G

2041
AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGAT
CTGC

128 K L I A Y P I A V E A L S L I Y N K D L

2101
TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGA
AAGCGA

148 L P N P P K T W E E I P A L D K E L K A

2161
AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCT
GATTG

168 K G K S A L M F N L Q E P Y F T W P L I

2221
CTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGA
CGTGG

188 A A D G G Y A F K Y E N G K Y D I K D V

2281
GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAA
AAACA

208 G V D N A G A K A G L T F L V D L I K N

2341
AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGG
CGAAA

228 K H M N A D T D Y S I A E A A F N K G E

2401
CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGT
GAATT

248 T A M T I N G P W A W S N I D T S K V N

2461
ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGG
CGTGC

268 Y G V T V L P T F K G Q P S K P F V G V

2521
TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCT
CGAAA

288 L S A G I N A A S P N K E L A K E F L E

2581
ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGG
TGCCG

308 N Y L L T D E G L E A V N K D K P L G A

2641
TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCAC
CATGG

328 V A L K S Y E E E L A K D P R I A A T M

Factor Xa PstI

2701

AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGC
CTCGG

348 E N A Q S A F W Y A V R I E A R L Q A S

SalI XbaI +2 trxA (2-109 del 103-107)

2761

TCGACGCCGAATCTAGAAGCGATAAAATTATTCACCTGACTGACGACAGTTTTGA
CACGG

368 V D A E S R S D K I I H L T D D S F D T

2821

ATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGG
TCCGT

388 D V L K A D G A I L V D F W A E W C G P

2881

GCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAACT
GACCG

408 C K M I A P I L D E I A D E Y Q G K L T

2941

TTGCAAAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCG
TGGTA

428 V A K L N I D Q N P G T A P K Y G I R G

3001

TCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGC
ACTGT

448 I P T L L L F K N G E V A A T K V G A L

FLAG

3061

CTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAATA
ATAAG

468 S K G Q L K E N L A D Y K D D D D K

Lost XbaI

CTAGAGG (transcriptional stop)

pMPX-71::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

Arabinose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-79 cut with PstI & XbaI.

SEQ ID NO.: 284

pMPX-92 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

5

SD Lost PstI +1 malE (1-370 del 354-364)

AGGAGGTTCTGCATATGAAAATAAAAACAGGTGCAC

10 1 M K I K T G A

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC AAAA

15 8 R I L A L S A L T T M M F S A S A L A K

TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCT CGCTG

20 28 I E E G K L V I W I N G D K G Y N G L A

AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCC GGATA

25 48 E V G K K F E K D T G I K V T V E H P D

AACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTAT
CTTCT

68 K L E E K F P Q V A A T G D G P D I I F

GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCAC
CCCGG

88 W A H D R F G G Y A Q S G L L A E I T P

ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAA
CGGCA

108 D K A F Q D K L Y P F T W D A V R Y N G

AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGAT
CTGC

128 K L I A Y P I A V E A L S L I Y N K D L

TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGA
AAGCGA

148 L P N P P K T W E E I P A L D K E L K A

AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCT
GATTG

168 K G K S A L M F N L Q E P Y F T W P L I

CTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGA
CGTGG

188 A A D G G Y A F K Y E N G K Y D I K D V

GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAA
AAACA

208 G V D N A G A K A G L T F L V D L I K N

2341
AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGG
CGAAA

228 K H M N A D T D Y S I A E A A F N K G E

2401
CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGT
GAATT

248 T A M T I N G P W A W S N I D T S K V N

2461

ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGG
CGTGC

268 Y G V T V L P T F K G Q P S K P F V G V

2521

TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCT
CGAAA

288 L S A G I N A A S P N K E L A K E F L E

2581

ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGG
TGCCG

308 N Y L L T D E G L E A V N K D K P L G A

2641

TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCAC
CATGG

328 V A L K S Y E E E L A K D P R I A A T M

Factor Xa PstI

2701

AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGC
CTCGG

348 E N A Q S A F W Y A V R I E A R L Q A S

SalI XbaI +2 trxA (2-109 del 103-107)

2761

TCGACGCCGAATCTAGAAGCGATAAAATTATTCACCTGACTGACGACAGTTTTGA
CACGG

368 V D A E S R S D K I I H L T D D S F D T

2821

ATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGG
TCCGT

388 D V L K A D G A I L V D F W A E W C G P

2881

GCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAACT
GACCG

408 C K M I A P I L D E I A D E Y Q G K L T

2941

TTGCAAAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCG
TGGTA

428 V A K L N I D Q N P G T A P K Y G I R G

3001

TCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGC
ACTGT

448 I P T L L L F K N G E V A A T K V G A L

5

FLAG

3061

CTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAATA
ATAAG

10 468 S K G Q L K E N L A D Y K D D D D K

Lost XbaI

CTAGAGGTACC (transcriptional stop)

15 pMPX-84::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI,
20 XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-90 cut with PstI & XbaI.

SEQ ID NO.: 285

pMPX-97 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1 malE (1-370 del 354-364)

AGGAGGTTCTGCATATGAAAATAAAAACAGGTGCAC

1 M K I K T G A

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC AAAA

8 R I L A L S A L T T M M F S A S A L A K

TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCT CGCTG

28 I E E G K L V I W I N G D K G Y N G L A

AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCC GGATA

48 E V G K K F E K D T G I K V T V E H P D

AACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTAT
CTTCT

68 K L E E K F P Q V A A T G D G P D I I F

GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCAC
CCCGG

88 W A H D R F G G Y A Q S G L L A E I T P

ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAA
CGGCA

108 D K A F Q D K L Y P F T W D A V R Y N G

AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGAT
CTGC

128 K L I A Y P I A V E A L S L I Y N K D L

TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGA
AAGCGA

148 L P N P P K T W E E I P A L D K E L K A

AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCT
GATTG

168 K G K S A L M F N L Q E P Y F T W P L I

CTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGA
CGTGG

188 A A D G G Y A F K Y E N G K Y D I K D V

GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAA
AAACA

208 G V D N A G A K A G L T F L V D L I K N

2341
AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGG
CGAAA

228 K H M N A D T D Y S I A E A A F N K G E

2401
CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGT
GAATT

248 T A M T I N G P W A W S N I D T S K V N

2461

ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGG
CGTGC

268 Y G V T V L P T F K G Q P S K P F V G V

2521

TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCT
CGAAA

288 L S A G I N A A S P N K E L A K E F L E

2581

ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGG
TGCCG

308 N Y L L T D E G L E A V N K D K P L G A

2641

TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCAC
CATGG

328 V A L K S Y E E E L A K D P R I A A T M

Factor Xa PstI

2701

AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGC
CTCGG

348 E N A Q S A F W Y A V R I E A R L Q A S

SalI XbaI +2 trxA (2-109 del 103-107)

2761

TCGACGCCGAATCTAGAAGCGATAAAATTATTCACCTGACTGACGACAGTTTTGA

CACGG

368 V D A E S R S D K I I H L T D D S F D T

2821

ATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGG

TCCGT

388 D V L K A D G A I L V D F W A E W C G P

2881

GCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAACT

GACCG

408 C K M I A P I L D E I A D E Y Q G K L T

2941

TTGCAAAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCG

TGGTA

428 V A K L N I D Q N P G T A P K Y G I R G

3001

TCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGC

ACTGT

448 I P T L L L F K N G E V A A T K V G A L

FLAG

3061

CTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAATA
ATAAG

468 S K G Q L K E N L A D Y K D D D D K

Lost XbaI

CTAGAGGTACC (transcriptional stop)

pMPX-86::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-95 cut with PstI & XbaI.

SEQ ID NO.: 151

pMPX-66 arabinose-inducible expression vector

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1       TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG
GAGACGGTCA
61      CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG
TCAGCGGGTG
```

121 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA
CTGAGAGTGC
181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC
ATCAGGCGCC
241 ATTCGCCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC
TCTTCGCTAT
301 TACGCCAGCT GGCGAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA
ACGCCAGGGT

HindIII
361 TTTCCCAGTC ACGACGTTGT AAAACGACGG CCAGTGCC**AA GCTT**CAAGCC
GTCAATTGTC

Stop araC
421 TGATTCGTTA CCAA**TTA**TGA CAACTTGACG GCTACATCAT TCACTTTTTC
TTCACAACCG

481 GCACGGAACT CGCTCGGGCT GGCCCCGGTG CATTTTTTAA ATACCCGCGA
GAAATAGAGT
541 TGATCGTCAA AACCAACATT GCGACCGACG GTGGCGATAG GCATCCGGGT
GGTGCTCAAA
601 AGCAGCTTCG CCTGGCTGAT ACGTTGGTCC TCGCGCCAGC TTAAGACGCT
AATCCCTAAC
661 TGCTGGCGGA AAAGATGTGA CAGACGCGAC GGCGACAAGC AAACATGCTG
TGCGACGCTG
721 GCGATATCAA AATTGCTGTC TGCCAGGTGA TCGCTGATGT ACTGACAAGC
CTCGCGTACC
781 CGATTATCCA TCGGTGGATG GAGCGACTCG TTAATCGCTT CCATGCGCCG
CAGTAACAAT
841 TGCTCAAGCA GATTTATCGC CAGCAGCTCC GAATAGCGCC CTTCCCCTTG
CCCGGCGTTA
901 ATGATTTGCC CAAACAGGTC GCTGAAATGC GGCTGGTGCG CTTCATCCGG
GCGAAAGAAC
961 CCCGTATTGG CAAATATTGA CGGCCAGTTA AGCCATTCAT GCCAGTAGGC
GCGCGGACGA
1021 AAGTAAACCC ACTGGTGATA CCATTCGCGA GCCTCCGGAT GACGACCGTA
GTGATGAATC
1081 TCTCCTGGCG GGAACAGCAA AATATCACCC GGTCGGCAAA CAAATTCTCG
TCCCTGATTT
1141 TTCACCACCC CCTGACCGCG AATGGTGAGA TTGAGAATAT AACCTTTCAT
TCCCAGCGGT
1201 CGGTCGATAA AAAAATCGAG ATAACCGTTG GCCTCAATCG GCGTTAAACC
CGCCACCAGA
1261 TGGGCATTAA ACGAGTATCC CGGCAGCAGG GGATCATTTT GCGCTTCAGC
CATACTTTTC

Start araC
1321 ATACTCCCGC CATTCAGAGA AGAAACCAAT TGTCCATATT G**CAT**CAGACA
TTGCCGTCAC
<--

1381 TGCGTCTTTT ACTGGCTCTT CTCGCTAACC AAACCGGTAA CCCCGCTTAT
TAAAAGCATT
1441 CTGTAACAAA GCGGGACCAA AGCCATGACA AAAACGCGTA ACAAAAGTGT
CTATAATCAC
1501 GGCAGAAAAG TCCACATTGA TTATTTGCAC GGCGTCACAC TTTGCTATGC
CATAGCATTT
1561 TTATCCATAA GATTAGCGGA TCCTACCTGA CGCTTTTTAT CGCAACTCTC
TACTGTTTCT

SD SalI XbaI
1621 CCATACCCGT TTTTTTGGGC TAGCAGGAGG CCGTCGACTC TAGAGGATCC
CCGCGCCCTC

Stem-loop KpnI
1681 ATCCGAAAGG GCGTATTGGT ACCGAGCTCG AATTCGTAAT CATGGTCATA
GCTGTTTCCT

1741 GTGTGAAATT GTTATCCGCT CACAATTCCA CACAACATAC GAGCCGGAAG
CATAAAGTGT
1801 AAAGCCTGGG GTGCCTAATG AGTGAGCTAA CTCACATTAA TTGCGTTGCG
CTCACTGCCC
1861 GCTTTCCAGT CGGGAAACCT GTCGTGCCAG CTGCATTAAT GAATCGGCCA
ACGCGCGGGG
1921 AGAGGCGGTT TGCGTATTGG GCGCTCTTCC GCTTCCTCGC TCACTGACTC
GCTGCGCTCG
1981 GTCGTTCGGC TGCGGCGAGC GGTATCAGCT CACTCAAAGG CGGTAATACG
GTTATCCACA
2041 GAATCAGGGG ATAACGCAGG AAAGAACATG TGAGCAAAAG GCCAGCAAAA
GGCCAGGAAC
2101 CGTAAAAAGG CCGCGTTGCT GGCGTTTTTC CATAGGCTCC GCCCCCCTGA
CGAGCATCAC
2161 AAAAATCGAC GCTCAAGTCA GAGGTGGCGA AACCCGACAG GACTATAAAG
ATACCAGGCG
2221 TTTCCCCCTG GAAGCTCCCT CGTGCGCTCT CCTGTTCCGA CCCTGCCGCT
TACCGGATAC
2281 CTGTCCGCCT TTCTCCCTTC GGGAAGCGTG GCGCTTTCTC ATAGCTCACG
CTGTAGGTAT
2341 CTCAGTTCGG TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG TGCACGAACC
CCCCGTTCAG
2401 CCCGACCGCT GCGCCTTATC CGGTAACTAT CGTCTTGAGT CCAACCCGGT
AAGACACGAC
2461 TTATCGCCAC TGGCAGCAGC CACTGGTAAC AGGATTAGCA GAGCGAGGTA
TGTAGGCGGT
2521 GCTACAGAGT TCTTGAAGTG GTGGCCTAAC TACGGCTACA CTAGAAGGAC
AGTATTTGGT
2581 ATCTGCGCTC TGCTGAAGCC AGTTACCTTC GGAAAAAGAG TTGGTAGCTC
TTGATCCGGC
2641 AAACAAACCA CCGCTGGTAG CGGTGGTTTT TTTGTTTGCA AGCAGCAGAT
TACGCGCAGA
2701 AAAAAAGGAT CTCAAGAAGA TCCTTTGATC TTTTCTACGG GGTCTGACGC
TCAGTGGAAC
2761 GAAAACTCAC GTTAAGGGAT TTTGGTCATG AGATTATCAA AAAGGATCTT
CACCTAGATC
2821 CTTTTAAATT AAAAATGAAG TTTTAAATCA ATCTAAAGTA TATATGAGTA
AACTTGGTCT
2881 GACAGTTACC AATGCTTAAT CAGTGAGGCA CCTATCTCAG CGATCTGTCT
ATTTCGTTCA
2941 TCCATAGTTG CCTGACTCCC CGTCGTGTAG ATAACTACGA TACGGGAGGG
CTTACCATCT
3001 GGCCCCAGTG CTGCAATGAT ACCGCGAGAC CCACGCTCAC CGGCTCCAGA
TTTATCAGCA
3061 ATAAACCAGC CAGCCGGAAG GGCCGAGCGC AGAAGTGGTC CTGCAACTTT
ATCCGCCTCC
3121 ATCCAGTCTA TTAATTGTTG CCGGGAAGCT AGAGTAAGTA GTTCGCCAGT
TAATAGTTTG
3181 CGCAACGTTG TTGCCATTGC TACAGGCATC GTGGTGTCAC GCTCGTCGTT
TGGTATGGCT

3241 TCATTCAGCT CCGGTTCCCA ACGATCAAGG CGAGTTACAT GATCCCCCAT
GTTGTGCAAA
3301 AAAGCGGTTA GCTCCTTCGG TCCTCCGATC GTTGTCAGAA GTAAGTTGGC
CGCAGTGTTA
3361 TCACTCATGG TTATGGCAGC ACTGCATAAT TCTCTTACTG TCATGCCATC
CGTAAGATGC
3421 TTTTCTGTGA CTGGTGAGTA CTCAACCAAG TCATTCTGAG AATAGTGTAT
GCGGCGACCG
3481 AGTTGCTCTT GCCCGGCGTC AATACGGGAT AATACCGCGC CACATAGCAG
AACTTTAAAA
3541 GTGCTCATCA TTGGAAAACG TTCTTCGGGG CGAAAACTCT CAAGGATCTT
ACCGCTGTTG
3601 AGATCCAGTT CGATGTAACC CACTCGTGCA CCCAACTGAT CTTCAGCATC
TTTTACTTTC
3661 ACCAGCGTTT CTGGGTGAGC AAAAACAGGA AGGCAAAATG CCGCAAAAAA
GGGAATAAGG
3721 GCGACACGGA AATGTTGAAT ACTCATACTC TTCCTTTTTC AATATTATTG
AAGCATTTAT
3781 CAGGGTTATT GTCTCATGAG CGGATACATA TTTGAATGTA TTTAGAAAAA
TAAACAAATA
3841 GGGGTTCCGC GCACATTTCC CCGAAAAGTG CCACCTGACG TCTAAGAAAC
CATTATTATC
3901 ATGACATTAA CCTATAAAAA TAGGCGTATC ACGAGGCCCT TTCGTC

The segment araC through Para was taken from pBAD24 using PCR added HindIII and modified aligned Shine-Delgarno (SD) sequence with SalI followed by XbaI, a stem-loop transcriptional stop sequence, and KpnI. The PCR product was cloned into pUC18 using HindIII and KpnI.

SEQ ID NO.: 152

pMPX-72 rhamnose-inducible expression vector

1 TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG
GAGACGGTCA
61 CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG
TCAGCGGGTG
121 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA
CTGAGAGTGC
181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC
ATCAGGCGCC
241 ATTCGCCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC
TCTTCGCTAT
301 TACGCCAGCT GGCGAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA
ACGCCAGGGT

Stop rhaR
361 TTTCCCAGTC ACGACGTTGT AAAACGACGG CCAGTGCCAA GCTTAATTAA
TCTTTCTGCG

HindIII

421 AATTGAGATG ACGCCACTGG CTGGGCGTCA TCCCGGTTTC CCGGGTAAAC
ACCACCGAAA
481 AATAGTTACT ATCTTCAAAG CCACATTCGG TCGAAATATC ACTGATTAAC
AGGCGGCTAT
541 GCTGGAGAAG ATATTGCGCA TGACACACTC TGACCTGTCG CAGATATTGA
TTGATGGTCA

601 TTCCAGTCTG CTGGCGAAAT TGCTGACGCA AAACGCGCTC ACTGCACGAT
GCCTCATCAC
661 AAAATTTATC CAGCGCAAAG GGACTTTTCA GGCTAGCCGC CAGCCGGGTA
ATCAGCTTAT
721 CCAGCAACGT TTCGCTGGAT GTTGGCGGCA ACGAATCACT GGTGTAACGA
TGGCGATTCA
781 GCAACATCAC CAACTGCCCG AACAGCAACT CAGCCATTTC GTTAGCAAAC
GGCACATGCT
841 GACTACTTTC ATGCTCAAGC TGACCGATAA CCTGCCGCGC CTGCGCCATC
CCCATGCTAC
901 CTAAGCGCCA GTGTGGTTGC CCTGCGCTGG CGTTAAATCC CGGAATCGCC
CCCTGCCAGT
961 CAAGATTCAG CTTCAGACGC TCCGGGCAAT AAATAATATT CTGCAAAACC
AGATCGTTAA
1021 CGGAAGCGTA GGAGTGTTTA TCGTCAGCAT GAATGTAAAA GAGATCGCCA
CGGGTAATGC
1081 GATAAGGGCG ATCGTTGAGT ACATGCAGGC CATTACCGCG CCAGACAATC
ACCAGCTCAC
1141 AAAAATCATG TGTATGTTCA GCAAAGACAT CTTGCGGATA ACGGTCAGCC
ACAGCGACTG
1201 CCTGCTGGTC GCTGGCAAAA AAATCATCTT TGAGAAGTTT TAACTGATGC
GCCACCGTGG
1261 CTACCTCGGC CAGAGAACGA AGTTGATTAT TCGCAATATG GCGTACAAAT
ACGTTGAGAA

Stop rhaS Start rhaR
1321 GATTCGCG**TT A**TTGCAGAAA GC**CAT**CCCGT CCCTGGCGAA TATCACGCGG
TGACCAGTTA
<--
1381 AACTCTCGGC GAAAAAGCGT CGAAAAGTGG TTACTGTCGC TGAATCCACA
GCGATAGGCG
1441 ATGTCAGTAA CGCTGGCCTC GCTGTGGCGT AGCAGATGTC GGGCTTTCAT
CAGTCGCAGG
1501 CGGTTCAGGT ATCGCTGAGG CGTCAGTCCC GTTTGCTGCT TAAGCTGCCG
ATGTAGCGTA
1561 CGCAGTGAAA GAGAAAATTG ATCCGCCACG GCATCCCAAT TCACCTCATC
GGCAAAATGG
1621 TCCTCCAGCC AGGCCAGAAG CAAGTTGAGA CGTGATGCGC TGTTTTCCAG
GTTCTCCTGC
1681 AAACTGCTTT TACGCAGCAA GAGCAGTAAT TGCATAAACA AGATCTCGCG
ACTGGCGGTC
1741 GAGGGTAAAT CATTTTCCCC TTCCTGCTGT TCCATCTGTG CAACCAGCTG
TCGCACCTGC
1801 TGCAATACGC TGTGGTTAAC GCGCCAGTGA GACGGATACT GCCCATCCAG
CTCTTGTGGC
1861 AGCAACTGAT TCAGCCCGGC GAGAAACTGA AATCGATCCG GCGAGCGATA
CAGCACATTG
1921 GTCAGACACA GATTATCGGT ATGTTCATAC AGATGCCGAT CATGATCGCG
TACGAAACAG
1981 ACCGTGCCAC CGGTGATGGT ATAGGGCTGC CCATTAAACA CATGAATACC
CGTGCCATGT
2041 TCGACAATCA CAATTTCATG AAAATCATGA TGATGTTCAG GAAAATCCGC
CTGCGGGAGC
2101 CGGGGTTCTA TCGCCACGGA CGCGTTACCA GACGGAAAAA AATCCACACT
ATGTAATACG

Start rhaS
2161 GT**CAT**ACTGG CCTCCTGATG TCGTCAACAC GGCGAAATAG TAATCACGAG
GTCAGGTTCT

<--

2221 TACCTTAAAT TTTCGACGGA AAACCACGTA AAAAACGTCG ATTTTTCAAG
ATACAGCGTG
2281 AATTTTCAGG AAATGCGGTG AGCATCACAT CACCACAATT CAGCAAATTG
TGAACATCAT
2341 CACGTTCATC TTTCCCTGGT TGCCAATGGC CCATTTTCCT GTCAGTAACG
AGAAGGTCGC

SD PstI SalI
2401 GAATTCAGGC GCTTTTTAGA CTGGTCGTAA TGAAATTCAG GAGGTTCTGC
AGGTCGACTC

XbaI Stem-loop KpnI
2461 TAGAGGATCC CCGCGCCCTC ATCCGAAAGG GCGTATTGGT ACCGAGCTCG
AATTCGTAAT

2521 CATGGTCATA GCTGTTTCCT GTGTGAAATT GTTATCCGCT CACAATTCCA
CACAACATAC
2581 GAGCCGGAAG CATAAAGTGT AAAGCCTGGG GTGCCTAATG AGTGAGCTAA
CTCACATTAA
2641 TTGCGTTGCG CTCACTGCCC GCTTTCCAGT CGGGAAACCT GTCGTGCCAG
CTGCATTAAT
2701 GAATCGGCCA ACGCGCGGGG AGAGGCGGTT TGCGTATTGG GCGCTCTTCC
GCTTCCTCGC
2761 TCACTGACTC GCTGCGCTCG GTCGTTCGGC TGCGGCGAGC GGTATCAGCT
CACTCAAAGG
2821 CGGTAATACG GTTATCCACA GAATCAGGGG ATAACGCAGG AAAGAACATG
TGAGCAAAAG
2881 GCCAGCAAAA GGCCAGGAAC CGTAAAAAGG CCGCGTTGCT GGCGTTTTTC
CATAGGCTCC
2941 GCCCCCCTGA CGAGCATCAC AAAAATCGAC GCTCAAGTCA GAGGTGGCGA
AACCCGACAG
3001 GACTATAAAG ATACCAGGCG TTTCCCCCTG GAAGCTCCCT CGTGCGCTCT
CCTGTTCCGA
3061 CCCTGCCGCT TACCGGATAC CTGTCCGCCT TTCTCCCTTC GGGAAGCGTG
GCGCTTTCTC
3121 ATAGCTCACG CTGTAGGTAT CTCAGTTCGG TGTAGGTCGT TCGCTCCAAG
CTGGGCTGTG
3181 TGCACGAACC CCCCGTTCAG CCCGACCGCT GCGCCTTATC CGGTAACTAT
CGTCTTGAGT
3241 CCAACCCGGT AAGACACGAC TTATCGCCAC TGGCAGCAGC CACTGGTAAC
AGGATTAGCA
3301 GAGCGAGGTA TGTAGGCGGT GCTACAGAGT TCTTGAAGTG GTGGCCTAAC
TACGGCTACA
3361 CTAGAAGGAC AGTATTTGGT ATCTGCGCTC TGCTGAAGCC AGTTACCTTC
GGAAAAAGAG
3421 TTGGTAGCTC TTGATCCGGC AAACAAACCA CCGCTGGTAG CGGTGGTTTT
TTTGTTTGCA
3481 AGCAGCAGAT TACGCGCAGA AAAAAAGGAT CTCAAGAAGA TCCTTTGATC
TTTTCTACGG
3541 GGTCTGACGC TCAGTGGAAC GAAAACTCAC GTTAAGGGAT TTTGGTCATG
AGATTATCAA
3601 AAAGGATCTT CACCTAGATC CTTTTAAATT AAAAATGAAG TTTTAAATCA
ATCTAAAGTA
3661 TATATGAGTA AACTTGGTCT GACAGTTACC AATGCTTAAT CAGTGAGGCA
CCTATCTCAG
3721 CGATCTGTCT ATTTCGTTCA TCCATAGTTG CCTGACTCCC CGTCGTGTAG
ATAACTACGA

3781 TACGGGAGGG CTTACCATCT GGCCCCAGTG CTGCAATGAT ACCGCGAGAC CCACGCTCAC
3841 CGGCTCCAGA TTTATCAGCA ATAAACCAGC CAGCCGGAAG GGCCGAGCGC AGAAGTGGTC
3901 CTGCAACTTT ATCCGCCTCC ATCCAGTCTA TTAATTGTTG CCGGGAAGCT AGAGTAAGTA
3961 GTTCGCCAGT TAATAGTTTG CGCAACGTTG TTGCCATTGC TACAGGCATC GTGGTGTCAC
4021 GCTCGTCGTT TGGTATGGCT TCATTCAGCT CCGGTTCCCA ACGATCAAGG CGAGTTACAT
4081 GATCCCCCAT GTTGTGCAAA AAAGCGGTTA GCTCCTTCGG TCCTCCGATC GTTGTCAGAA
4141 GTAAGTTGGC CGCAGTGTTA TCACTCATGG TTATGGCAGC ACTGCATAAT TCTCTTACTG
4201 TCATGCCATC CGTAAGATGC TTTTCTGTGA CTGGTGAGTA CTCAACCAAG TCATTCTGAG
4261 AATAGTGTAT GCGGCGACCG AGTTGCTCTT GCCCGGCGTC AATACGGGAT AATACCGCGC
4321 CACATAGCAG AACTTTAAAA GTGCTCATCA TTGGAAAACG TTCTTCGGGG CGAAAACTCT
4381 CAAGGATCTT ACCGCTGTTG AGATCCAGTT CGATGTAACC CACTCGTGCA CCCAACTGAT
4441 CTTCAGCATC TTTTACTTTC ACCAGCGTTT CTGGGTGAGC AAAAACAGGA AGGCAAAATG
4501 CCGCAAAAAA GGGAATAAGG GCGACACGGA AATGTTGAAT ACTCATACTC TTCCTTTTTC
4561 AATATTATTG AAGCATTTAT CAGGGTTATT GTCTCATGAG CGGATACATA TTTGAATGTA
4621 TTTAGAAAAA TAAACAAATA GGGGTTCCGC GCACATTTCC CCGAAAAGTG CCACCTGACG
4681 TCTAAGAAAC CATTATTATC ATGACATTAA CCTATAAAAA TAGGCGTATC ACGAGGCCCT
4741 TTCGTC

The segment rhaR through Prha was taken from the E. coli chromosome using PCR added HindIII and modified aligned Shine-Delgarno (SD) sequence with PstI followed by SalI, XbaI, a stem-loop transcriptional stop sequence, and KpnI. The PCR product was cloned into pUC18 using HindIII and KpnI.

SEQ ID NO.: 153

pMPX-67 rhamnose-inducible expression vector

1 TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA
61 CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGCGGGTG
121 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC
181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGGCGCC
241 ATTCGCCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC TCTTCGCTAT
301 TACGCCAGCT GGCGAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA ACGCCAGGGT

Stop rhaR

361 TTTCCCAGTC ACGACGTTGT AAAACGACGG CCAGTGCCAA GC**TTA**ATTAA
TCTTTCTGCG

HindIII

421 AATTGAGATG ACGCCACTGG CTGGGCGTCA TCCCGGTTTC CCGGGTAAAC
ACCACCGAAA
481 AATAGTTACT ATCTTCAAAG CCACATTCGG TCGAAATATC ACTGATTAAC
AGGCGGCTAT
541 GCTGGAGAAG ATATTGCGCA TGACACACTC TGACCTGTCG CAGATATTGA
TTGATGGTCA
601 TTCCAGTCTG CTGGCGAAAT TGCTGACGCA AAACGCGCTC ACTGCACGAT
GCCTCATCAC
661 AAAATTTATC CAGCGCAAAG GGACTTTTCA GGCTAGCCGC CAGCCGGGTA
ATCAGCTTAT
721 CCAGCAACGT TTCGCTGGAT GTTGGCGGCA ACGAATCACT GGTGTAACGA
TGGCGATTCA
781 GCAACATCAC CAACTGCCCG AACAGCAACT CAGCCATTTC GTTAGCAAAC
GGCACATGCT
841 GACTACTTTC ATGCTCAAGC TGACCGATAA CCTGCCGCGC CTGCGCCATC
CCCATGCTAC
901 CTAAGCGCCA GTGTGGTTGC CCTGCGCTGG CGTTAAATCC CGGAATCGCC
CCCTGCCAGT
961 CAAGATTCAG CTTCAGACGC TCCGGGCAAT AAATAATATT CTGCAAAACC
AGATCGTTAA
1021 CGGAAGCGTA GGAGTGTTTA TCGTCAGCAT GAATGTAAAA GAGATCGCCA
CGGGTAATGC
1081 GATAAGGGCG ATCGTTGAGT ACATGCAGGC CATTACCGCG CCAGACAATC
ACCAGCTCAC
1141 AAAAATCATG TGTATGTTCA GCAAAGACAT CTTGCGGATA ACGGTCAGCC
ACAGCGACTG
1201 CCTGCTGGTC GCTGGCAAAA AAATCATCTT TGAGAAGTTT TAACTGATGC
GCCACCGTGG
1261 CTACCTCGGC CAGAGAACGA AGTTGATTAT TCGCAATATG GCGTACAAAT
ACGTTGAGAA

Stop rhaS Start rhaR

1321 GATTCGCG**TT A**TTGCAGAAA GC**CAT**CCCGT CCCTGGCGAA TATCACGCGG
TGACCAGTTA

<---

1381 AACTCTCGGC GAAAAAGCGT CGAAAAGTGG TTACTGTCGC TGAATCCACA
GCGATAGGCG
1441 ATGTCAGTAA CGCTGGCCTC GCTGTGGCGT AGCAGATGTC GGGCTTTCAT
CAGTCGCAGG
1501 CGGTTCAGGT ATCGCTGAGG CGTCAGTCCC GTTTGCTGCT TAAGCTGCCG
ATGTAGCGTA
1561 CGCAGTGAAA GAGAAAATTG ATCCGCCACG GCATCCCAAT TCACCTCATC
GGCAAAATGG
1621 TCCTCCAGCC AGGCCAGAAG CAAGTTGAGA CGTGATGCGC TGTTTTCCAG
GTTCTCCTGC
1681 AAACTGCTTT TACGCAGCAA GAGCAGTAAT TGCATAAACA AGATCTCGCG
ACTGGCGGTC
1741 GAGGGTAAAT CATTTTCCCC TTCCTGCTGT TCCATCTGTG CAACCAGCTG
TCGCACCTGC
1801 TGCAATACGC TGTGGTTAAC GCGCCAGTGA GACGGATACT GCCCATCCAG
CTCTTGTGGC
1861 AGCAACTGAT TCAGCCCGGC GAGAAACTGA AATCGATCCG GCGAGCGATA
CAGCACATTG

1921 GTCAGACACA GATTATCGGT ATGTTCATAC AGATGCCGAT CATGATCGCG
TACGAAACAG
1981 ACCGTGCCAC CGGTGATGGT ATAGGGCTGC CCATTAAACA CATGAATACC
CGTGCCATGT
2041 TCGACAATCA CAATTTCATG AAAATCATGA TGATGTTCAG GAAAATCCGC
CTGCGGGAGC
2101 CGGGGTTCTA TCGCCACGGA CGCGTTACCA GACGGAAAAA AATCCACACT
ATGTAATACG

Start rhaS
2161 GT**CAT**ACTGG CCTCCTGATG TCGTCAACAC GGCGAAATAG TAATCACGAG
GTCAGGTTCT
<--

2221 TACCTTAAAT TTTCGACGGA AAACCACGTA AAAAACGTCG ATTTTTCAAG
ATACAGCGTG
2281 AATTTTCAGG AAATGCGGTG AGCATCACAT CACCACAATT CAGCAAATTG
TGAACATCAT
2341 CACGTTCATC TTTCCCTGGT TGCCAATGGC CCATTTTCCT GTCAGTAACG
AGAAGGTCGC

SD SalI XbaI

2401 GAATTCAGGC GCTTTTTAGA CTGGTCGTAA TGAAATTC**AG GAGG**TTGTCG
AC**TCTAGA**GG

Stem-loop KpnI
2461 ATCCCCGCGC CCTCATCCGA AAGGGCGTAT T**GGTACC**GAG CTCGAATTCG
TAATCATGGT

2521 CATAGCTGTT TCCTGTGTGA AATTGTTATC CGCTCACAAT TCCACACAAC
ATACGAGCCG
2581 GAAGCATAAA GTGTAAAGCC TGGGGTGCCT AATGAGTGAG CTAACTCACA
TTAATTGCGT
2641 TGCGCTCACT GCCCGCTTTC CAGTCGGGAA ACCTGTCGTG CCAGCTGCAT
TAATGAATCG
2701 GCCAACGCGC GGGGAGAGGC GGTTTGCGTA TTGGGCGCTC TTCCGCTTCC
TCGCTCACTG
2761 ACTCGCTGCG CTCGGTCGTT CGGCTGCGGC GAGCGGTATC AGCTCACTCA
AAGGCGGTAA
2821 TACGGTTATC CACAGAATCA GGGGATAACG CAGGAAAGAA CATGTGAGCA
AAAGGCCAGC
2881 AAAAGGCCAG GAACCGTAAA AAGGCCGCGT TGCTGGCGTT TTTCCATAGG
CTCCGCCCCC
2941 CTGACGAGCA TCACAAAAAT CGACGCTCAA GTCAGAGGTG GCGAAACCCG
ACAGGACTAT
3001 AAAGATACCA GGCGTTTCCC CCTGGAAGCT CCCTCGTGCG CTCTCCTGTT
CCGACCCTGC
3061 CGCTTACCGG ATACCTGTCC GCCTTTCTCC CTTCGGGAAG CGTGGCGCTT
TCTCATAGCT
3121 CACGCTGTAG GTATCTCAGT TCGGTGTAGG TCGTTCGCTC CAAGCTGGGC
TGTGTGCACG
3181 AACCCCCCGT TCAGCCCGAC CGCTGCGCCT TATCCGGTAA CTATCGTCTT
GAGTCCAACC
3241 CGGTAAGACA CGACTTATCG CCACTGGCAG CAGCCACTGG TAACAGGATT
AGCAGAGCGA
3301 GGTATGTAGG CGGTGCTACA GAGTTCTTGA AGTGGTGGCC TAACTACGGC
TACACTAGAA

3361 GGACAGTATT TGGTATCTGC GCTCTGCTGA AGCCAGTTAC CTTCGGAAAA
AGAGTTGGTA
3421 GCTCTTGATC CGGCAAACAA ACCACCGCTG GTAGCGGTGG TTTTTTTGTT
TGCAAGCAGC
3481 AGATTACGCG CAGAAAAAAA GGATCTCAAG AAGATCCTTT GATCTTTTCT
ACGGGGTCTG
3541 ACGCTCAGTG GAACGAAAAC TCACGTTAAG GGATTTTGGT CATGAGATTA
TCAAAAAGGA
3601 TCTTCACCTA GATCCTTTTA AATTAAAAAT GAAGTTTTAA ATCAATCTAA
AGTATATATG
3661 AGTAAACTTG GTCTGACAGT TACCAATGCT TAATCAGTGA GGCACCTATC
TCAGCGATCT
3721 GTCTATTTCG TTCATCCATA GTTGCCTGAC TCCCCGTCGT GTAGATAACT
ACGATACGGG
3781 AGGGCTTACC ATCTGGCCCC AGTGCTGCAA TGATACCGCG AGACCCACGC
TCACCGGCTC
3841 CAGATTTATC AGCAATAAAC CAGCCAGCCG GAAGGGCCGA GCGCAGAAGT
GGTCCTGCAA
3901 CTTTATCCGC CTCCATCCAG TCTATTAATT GTTGCCGGGA AGCTAGAGTA
AGTAGTTCGC
3961 CAGTTAATAG TTTGCGCAAC GTTGTTGCCA TTGCTACAGG CATCGTGGTG
TCACGCTCGT
4021 CGTTTGGTAT GGCTTCATTC AGCTCCGGTT CCCAACGATC AAGGCGAGTT
ACATGATCCC
4081 CCATGTTGTG CAAAAAAGCG GTTAGCTCCT TCGGTCCTCC GATCGTTGTC
AGAAGTAAGT
4141 TGGCCGCAGT GTTATCACTC ATGGTTATGG CAGCACTGCA TAATTCTCTT
ACTGTCATGC
4201 CATCCGTAAG ATGCTTTTCT GTGACTGGTG AGTACTCAAC CAAGTCATTC
TGAGAATAGT
4261 GTATGCGGCG ACCGAGTTGC TCTTGCCCGG CGTCAATACG GGATAATACC
GCGCCACATA
4321 GCAGAACTTT AAAAGTGCTC ATCATTGGAA AACGTTCTTC GGGGCGAAAA
CTCTCAAGGA
4381 TCTTACCGCT GTTGAGATCC AGTTCGATGT AACCCACTCG TGCACCCAAC
TGATCTTCAG
4441 CATCTTTTAC TTTCACCAGC GTTTCTGGGT GAGCAAAAAC AGGAAGGCAA
AATGCCGCAA
4501 AAAAGGGAAT AAGGGCGACA CGGAAATGTT GAATACTCAT ACTCTTCCTT
TTTCAATATT
4561 ATTGAAGCAT TTATCAGGGT TATTGTCTCA TGAGCGGATA CATATTTGAA
TGTATTTAGA
4621 AAAATAAACA AATAGGGGTT CCGCGCACAT TTCCCCGAAA AGTGCCACCT
GACGTCTAAG
4681 AAACCATTAT TATCATGACA TTAACCTATA AAAATAGGCG TATCACGAGG
CCCTTTCGTC

The segment rhaR through Prha was taken from the E. coli chromosome using PCR added HindIII and modified aligned Shine-Delgarno (SD) sequence with SalI followed by XbaI, a stem-loop transcriptional stop sequence, and KpnI. The PCR product was cloned into pUC18 using HindIII and KpnI.

SEQ ID NO.: 154

pMPX-71 arabinose-inducible expression vector

```
1       TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG
GAGACGGTCA
61      CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG
TCAGCGGGTG
121     TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA
CTGAGAGTGC
181     ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC
ATCAGGCGCC
241     ATTCGCCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC
TCTTCGCTAT
301     TACGCCAGCT GGCGAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA
ACGCCAGGGT

                                                    HindIII
361     TTTCCCAGTC ACGACGTTGT AAAACGACGG CCAGTGCCAA GCTTCAAGCC
GTCAATTGTC

                        Stop araC
421     TGATTCGTTA CCAATTATGA CAACTTGACG GCTACATCAT TCACTTTTTC
TTCACAACCG
481     GCACGGAACT CGCTCGGGCT GGCCCCGGTG CATTTTTTAA ATACCCGCGA
GAAATAGAGT
541     TGATCGTCAA AACCAACATT GCGACCGACG GTGGCGATAG GCATCCGGGT
GGTGCTCAAA
601     AGCAGCTTCG CCTGGCTGAT ACGTTGGTCC TCGCGCCAGC TTAAGACGCT
AATCCCTAAC
661     TGCTGGCGGA AAAGATGTGA CAGACGCGAC GGCGACAAGC AAACATGCTG
TGCGACGCTG
721     GCGATATCAA AATTGCTGTC TGCCAGGTGA TCGCTGATGT ACTGACAAGC
CTCGCGTACC
781     CGATTATCCA TCGGTGGATG GAGCGACTCG TTAATCGCTT CCATGCGCCG
CAGTAACAAT
841     TGCTCAAGCA GATTTATCGC CAGCAGCTCC GAATAGCGCC CTTCCCCTTG
CCCGGCGTTA
901     ATGATTTGCC CAAACAGGTC GCTGAAATGC GGCTGGTGCG CTTCATCCGG
GCGAAAGAAC
961     CCCGTATTGG CAAATATTGA CGGCCAGTTA AGCCATTCAT GCCAGTAGGC
GCGCGGACGA
1021    AAGTAAACCC ACTGGTGATA CCATTCGCGA GCCTCCGGAT GACGACCGTA
GTGATGAATC
1081    TCTCCTGGCG GGAACAGCAA AATATCACCC GGTCGGCAAA CAAATTCTCG
TCCCTGATTT
1141    TTCACCACCC CCTGACCGCG AATGGTGAGA TTGAGAATAT AACCTTTCAT
TCCCAGCGGT
1201    CGGTCGATAA AAAAATCGAG ATAACCGTTG GCCTCAATCG GCGTTAAACC
CGCCACCAGA
1261    TGGGCATTAA ACGAGTATCC CGGCAGCAGG GGATCATTTT GCGCTTCAGC
CATACTTTTC

                                                  Start araC
1321    ATACTCCCGC CATTCAGAGA AGAAACCAAT TGTCCATATT GCATCAGACA
TTGCCGTCAC
                                                        <--
1381    TGCGTCTTTT ACTGGCTCTT CTCGCTAACC AAACCGGTAA CCCCGCTTAT
TAAAAGCATT
1441    CTGTAACAAA GCGGGACCAA AGCCATGACA AAAACGCGTA ACAAAAGTGT
CTATAATCAC
1501    GGCAGAAAAG TCCACATTGA TTATTTGCAC GGCGTCACAC TTTGCTATGC
CATAGCATTT
```

1561 TTATCCATAA GATTAGCGGA TCCTACCTGA CGCTTTTTAT CGCAACTCTC
TACTGTTTCT

SD PstI SalI XbaI
1621 CCATACCCGT TTTTTTGGGC TAGC**AGGAGG** CC**CTGCAG**GT CGAC**TCTAGA**
GGATCCCCGC

Stem-loop KpnI
1681 GCCCTCATCC GAAAGGGCGT ATT**GGTACC**G AGCTCGAATT CGTAATCATG
GTCATAGCTG

1741 TTTCCTGTGT GAAATTGTTA TCCGCTCACA ATTCCACACA ACATACGAGC
CGGAAGCATA
1801 AAGTGTAAAG CCTGGGGTGC CTAATGAGTG AGCTAACTCA CATTAATTGC
GTTGCGCTCA
1861 CTGCCCGCTT TCCAGTCGGG AAACCTGTCG TGCCAGCTGC ATTAATGAAT
CGGCCAACGC
1921 GCGGGGAGAG GCGGTTTGCG TATTGGGCGC TCTTCCGCTT CCTCGCTCAC
TGACTCGCTG
1981 CGCTCGGTCG TTCGGCTGCG GCGAGCGGTA TCAGCTCACT CAAAGGCGGT
AATACGGTTA
2041 TCCACAGAAT CAGGGGATAA CGCAGGAAAG AACATGTGAG CAAAAGGCCA
GCAAAAGGCC
2101 AGGAACCGTA AAAAGGCCGC GTTGCTGGCG TTTTTCCATA GGCTCCGCCC
CCCTGACGAG
2161 CATCACAAAA ATCGACGCTC AAGTCAGAGG TGGCGAAACC CGACAGGACT
ATAAAGATAC
2221 CAGGCGTTTC CCCCTGGAAG CTCCCTCGTG CGCTCTCCTG TTCCGACCCT
GCCGCTTACC
2281 GGATACCTGT CCGCCTTTCT CCCTTCGGGA AGCGTGGCGC TTTCTCATAG
CTCACGCTGT
2341 AGGTATCTCA GTTCGGTGTA GGTCGTTCGC TCCAAGCTGG GCTGTGTGCA
CGAACCCCCC
2401 GTTCAGCCCG ACCGCTGCGC CTTATCCGGT AACTATCGTC TTGAGTCCAA
CCCGGTAAGA
2461 CACGACTTAT CGCCACTGGC AGCAGCCACT GGTAACAGGA TTAGCAGAGC
GAGGTATGTA
2521 GGCGGTGCTA CAGAGTTCTT GAAGTGGTGG CCTAACTACG GCTACACTAG
AAGGACAGTA
2581 TTTGGTATCT GCGCTCTGCT GAAGCCAGTT ACCTTCGGAA AAAGAGTTGG
TAGCTCTTGA
2641 TCCGGCAAAC AAACCACCGC TGGTAGCGGT GGTTTTTTTG TTTGCAAGCA
GCAGATTACG
2701 CGCAGAAAAA AAGGATCTCA AGAAGATCCT TTGATCTTTT CTACGGGGTC
TGACGCTCAG
2761 TGGAACGAAA ACTCACGTTA AGGGATTTTG GTCATGAGAT TATCAAAAAG
GATCTTCACC
2821 TAGATCCTTT TAAATTAAAA ATGAAGTTTT AAATCAATCT AAAGTATATA
TGAGTAAACT
2881 TGGTCTGACA GTTACCAATG CTTAATCAGT GAGGCACCTA TCTCAGCGAT
CTGTCTATTT
2941 CGTTCATCCA TAGTTGCCTG ACTCCCCGTC GTGTAGATAA CTACGATACG
GGAGGGCTTA
3001 CCATCTGGCC CCAGTGCTGC AATGATACCG CGAGACCCAC GCTCACCGGC
TCCAGATTTA
3061 TCAGCAATAA ACCAGCCAGC CGGAAGGGCC GAGCGCAGAA GTGGTCCTGC
AACTTTATCC
3121 GCCTCCATCC AGTCTATTAA TTGTTGCCGG GAAGCTAGAG TAAGTAGTTC
GCCAGTTAAT

3181 AGTTTGCGCA ACGTTGTTGC CATTGCTACA GGCATCGTGG TGTCACGCTC
GTCGTTTGGT
3241 ATGGCTTCAT TCAGCTCCGG TTCCCAACGA TCAAGGCGAG TTACATGATC
CCCCATGTTG
3301 TGCAAAAAAG CGGTTAGCTC CTTCGGTCCT CCGATCGTTG TCAGAAGTAA
GTTGGCCGCA
3361 GTGTTATCAC TCATGGTTAT GGCAGCACTG CATAATTCTC TTACTGTCAT
GCCATCCGTA
3421 AGATGCTTTT CTGTGACTGG TGAGTACTCA ACCAAGTCAT TCTGAGAATA
GTGTATGCGG
3481 CGACCGAGTT GCTCTTGCCC GGCGTCAATA CGGGATAATA CCGCGCCACA
TAGCAGAACT
3541 TTAAAAGTGC TCATCATTGG AAAACGTTCT TCGGGGCGAA AACTCTCAAG
GATCTTACCG
3601 CTGTTGAGAT CCAGTTCGAT GTAACCCACT CGTGCACCCA ACTGATCTTC
AGCATCTTTT
3661 ACTTTCACCA GCGTTTCTGG GTGAGCAAAA ACAGGAAGGC AAAATGCCGC
AAAAAAGGGA
3721 ATAAGGGCGA CACGGAAATG TTGAATACTC ATACTCTTCC TTTTTCAATA
TTATTGAAGC
3781 ATTTATCAGG GTTATTGTCT CATGAGCGGA TACATATTTG AATGTATTTA
GAAAAATAAA
3841 CAAATAGGGG TTCCGCGCAC ATTTCCCCGA AAAGTGCCAC CTGACGTCTA
AGAAACCATT
3901 ATTATCATGA CATTAACCTA TAAAAATAGG CGTATCACGA GGCCCTTTCG TC

The segment araC through Para was taken from pBAD24 using PCR added HindIII and modified aligned Shine-Delgarno (SD) sequence with PstI followed by SalI, XbaI, a stem-loop transcriptional stop sequence, and KpnI. The PCR product was cloned into pUC18 using HindIII and KpnI.

SEQ ID NO.: 155

pMPX-68 melibiose-inducible expression vector

1 TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG
GAGACGGTCA
61 CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG
TCAGCGGGTG
121 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA
CTGAGAGTGC
181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC
ATCAGGCGCC
241 ATTCGCCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC
TCTTCGCTAT
301 TACGCCAGCT GGCGAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA
ACGCCAGGGT

HindIII
361 TTTCCCAGTC ACGACGTTGT AAAACGACGG CCAGTGCC**AA GCTTTTA**GCC
GGGAAACGTC

Stop MelR

421 TGGCGGCGCT GTTGGCTAAG TTTGCGGTAT TGTTGCGGCG ACATGCCGAC
ATATTTGCCG
481 AACGTGCTGT AAAAACGACT ACTTGAACGA AAGCCTGCCG TCAGGGCAAT
ATCGAGAATA

541 CTTTTATCGG TATCGCTCAG TAACGCGCGA ACGTGGTTGA TGCGCATCGC
GGTAATGTAC
601 TGTTTCATCG TCAATTGCAT GACCCGCTGG AATATCCCCA TTGCATAGTT
GGCGTTAAGT
661 TTGACGTGCT CAGCCACATC GTTGATGGTC AGCGCCTGAT CATAGTTTTC
GGCAATAAAG
721 CCCAGCATCT GGCTAACATA AAATTGCGCA TGGCGCGAGA CGCTGTTTTT
GTGTGTGCGC
781 GAGGTTTTAT TGACCAGAAT CGGTTCCCAG CCAGAGAGGC TAAATCGCTT
GAGCATCAGG
841 CCAATTTCAT CAATGGCGAG CTGGCGAATT TGCTCGTTCG GACTGTTTAA
TTCCTGCTGC
901 CAGCGGCGCA CTTCAAACGG GCTAAGTTGC TGTGTGGCCA GTGATTTGAT
CACCATGCCG
961 TGAGTGACGT GGTTAATCAG GTCTTTATCC AGCGGCCAGG AGAGAAACAG
ATGCATCGGC
1021 AGATTAAAAA TCGCCATGCT CTGACAGGTT CCGGTATCTG TTAGTTGGTG
CGGTGTACAG
1081 GCCCAGAACA GCGTGATATG ACCCTGATTG ATATTCACTT TTTCATTGTT
GATCAGGTAT
1141 TCCACATCGC CATCGAAAGG CACATTCACT TCGACCTGAC CATGCCAGTG
GCTGGTGGGC
1201 ATGATATGCG GTGCGCGAAA CTCAATCTCC ATCCGCTGGT ATTCCGAATA
CAGCGACAGC

+1 MelR

1261 GGGCTGCGGG TCTGTTTTTC GTCGCTGCTG CACATAAACG TATCTGTATT
CATGGATGGC

1321 TCTCTTTCCT GGAATATCAG AATTATGGCA GGAGTGAGGG AGGATGACTG
CGAGTGGGAG
1381 CACGGTTTTC ACCCTCTTCC CAGAGGGGCG AGGGGACTCT CCGAGTATCA
TGAGGCCGAA
1441 AACTCTGCTT TTCAGGTAAT TTATTCCCAT AAACTCAGAT TTACTGCTGC
TTCACGCAGG
1501 ATCTGAGTTT ATGGGAATGC TCAACCTGGA AGCCGGAGGT TTTCTGCAGA
TTCGCCTGCC

SD SalI XbaI

1561 ATGATGAAGT TATTCAAGCA AGCCAGGAGG TC**GTCGAC**TC TAGAGGATCC
CCGCGCCCTC

Stem-loop KpnI

1621 ATCCGAAAGG GCGTATT**GGT ACC**GAGCTCG AATTCGTAAT CATGGTCATA
GCTGTTTCCT

1681 GTGTGAAATT GTTATCCGCT CACAATTCCA CACAACATAC GAGCCGGAAG
CATAAAGTGT
1741 AAAGCCTGGG GTGCCTAATG AGTGAGCTAA CTCACATTAA TTGCGTTGCG
CTCACTGCCC
1801 GCTTTCCAGT CGGGAAACCT GTCGTGCCAG CTGCATTAAT GAATCGGCCA
ACGCGCGGGG
1861 AGAGGCGGTT TGCGTATTGG GCGCTCTTCC GCTTCCTCGC TCACTGACTC
GCTGCGCTCG
1921 GTCGTTCGGC TGCGGCGAGC GGTATCAGCT CACTCAAAGG CGGTAATACG
GTTATCCACA
1981 GAATCAGGGG ATAACGCAGG AAAGAACATG TGAGCAAAAG GCCAGCAAAA
GGCCAGGAAC

2041 CGTAAAAAGG CCGCGTTGCT GGCGTTTTTC CATAGGCTCC GCCCCCCTGA
CGAGCATCAC
2101 AAAAATCGAC GCTCAAGTCA GAGGTGGCGA AACCCGACAG GACTATAAAG
ATACCAGGCG
2161 TTTCCCCCTG GAAGCTCCCT CGTGCGCTCT CCTGTTCCGA CCCTGCCGCT
TACCGGATAC
2221 CTGTCCGCCT TTCTCCCTTC GGGAAGCGTG GCGCTTTCTC ATAGCTCACG
CTGTAGGTAT
2281 CTCAGTTCGG TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG TGCACGAACC
CCCCGTTCAG
2341 CCCGACCGCT GCGCCTTATC CGGTAACTAT CGTCTTGAGT CCAACCCGGT
AAGACACGAC
2401 TTATCGCCAC TGGCAGCAGC CACTGGTAAC AGGATTAGCA GAGCGAGGTA
TGTAGGCGGT
2461 GCTACAGAGT TCTTGAAGTG GTGGCCTAAC TACGGCTACA CTAGAAGGAC
AGTATTTGGT
2521 ATCTGCGCTC TGCTGAAGCC AGTTACCTTC GGAAAAAGAG TTGGTAGCTC
TTGATCCGGC
2581 AAACAAACCA CCGCTGGTAG CGGTGGTTTT TTTGTTTGCA AGCAGCAGAT
TACGCGCAGA
2641 AAAAAAGGAT CTCAAGAAGA TCCTTTGATC TTTTCTACGG GGTCTGACGC
TCAGTGGAAC
2701 GAAAACTCAC GTTAAGGGAT TTTGGTCATG AGATTATCAA AAAGGATCTT
CACCTAGATC
2761 CTTTTAAATT AAAAATGAAG TTTTAAATCA ATCTAAAGTA TATATGAGTA
AACTTGGTCT
2821 GACAGTTACC AATGCTTAAT CAGTGAGGCA CCTATCTCAG CGATCTGTCT
ATTTCGTTCA
2881 TCCATAGTTG CCTGACTCCC CGTCGTGTAG ATAACTACGA TACGGGAGGG
CTTACCATCT
2941 GGCCCCAGTG CTGCAATGAT ACCGCGAGAC CCACGCTCAC CGGCTCCAGA
TTTATCAGCA
3001 ATAAACCAGC CAGCCGGAAG GGCCGAGCGC AGAAGTGGTC CTGCAACTTT
ATCCGCCTCC
3061 ATCCAGTCTA TTAATTGTTG CCGGGAAGCT AGAGTAAGTA GTTCGCCAGT
TAATAGTTTG
3121 CGCAACGTTG TTGCCATTGC TACAGGCATC GTGGTGTCAC GCTCGTCGTT
TGGTATGGCT
3181 TCATTCAGCT CCGGTTCCCA ACGATCAAGG CGAGTTACAT GATCCCCCAT
GTTGTGCAAA
3241 AAAGCGGTTA GCTCCTTCGG TCCTCCGATC GTTGTCAGAA GTAAGTTGGC
CGCAGTGTTA
3301 TCACTCATGG TTATGGCAGC ACTGCATAAT TCTCTTACTG TCATGCCATC
CGTAAGATGC
3361 TTTTCTGTGA CTGGTGAGTA CTCAACCAAG TCATTCTGAG AATAGTGTAT
GCGGCGACCG
3421 AGTTGCTCTT GCCCGGCGTC AATACGGGAT AATACCGCGC CACATAGCAG
AACTTTAAAA
3481 GTGCTCATCA TTGGAAAACG TTCTTCGGGG CGAAAACTCT CAAGGATCTT
ACCGCTGTTG
3541 AGATCCAGTT CGATGTAACC CACTCGTGCA CCCAACTGAT CTTCAGCATC
TTTTACTTTC
3601 ACCAGCGTTT CTGGGTGAGC AAAAACAGGA AGGCAAAATG CCGCAAAAAA
GGGAATAAGG
3661 GCGACACGGA AATGTTGAAT ACTCATACTC TTCCTTTTTC AATATTATTG
AAGCATTTAT
3721 CAGGGTTATT GTCTCATGAG CGGATACATA TTTGAATGTA TTTAGAAAAA
TAAACAAATA
3781 GGGGTTCCGC GCACATTTCC CCGAAAAGTG CCACCTGACG TCTAAGAAAC
CATTATTATC

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3841   ATGACATTAA CCTATAAAAA TAGGCGTATC ACGAGGCCCT TTCGTC
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SEQ ID NO.: 166

MalE (1-370) Factor Xa NTR (43-424) FLAG

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      SalI +1  MalE (1-370)
1   GTCGACATGAAAATAAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTT
1          M  K  I  K  T  G  A  R  I  L  A  L  S  A  L  T  T  M  M  F

61      TCCGCCTCGGCTCTCGCCAAAATCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGAT
21       S  A  S  A  L  A  K  I  E  E  G  K  L  V  I  W  I  N  G  D

121     AAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAA
41       K  G  Y  N  G  L  A  E  V  G  K  K  F  E  K  D  T  G  I  K

181     GTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGC
61       V  T  V  E  H  P  D  K  L  E  E  K  F  P  Q  V  A  A  T  G

241     GATGGCCCTGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGC
81       D  G  P  D  I  I  F  W  A  H  D  R  F  G  G  Y  A  Q  S  G

301     CTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGG
101      L  L  A  E  I  T  P  D  K  A  F  Q  D  K  L  Y  P  F  T  W

361     GATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCG
121      D  A  V  R  Y  N  G  K  L  I  A  Y  P  I  A  V  E  A  L  S

421     CTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCG
141      L  I  Y  N  K  D  L  L  P  N  P  P  K  T  W  E  E  I  P  A

481     CTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCG
161      L  D  K  E  L  K  A  K  G  K  S  A  L  M  F  N  L  Q  E  P

541     TACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGC
181      Y  F  T  W  P  L  I  A  A  D  G  G  Y  A  F  K  Y  E  N  G

601     AAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTC
201      K  Y  D  I  K  D  V  G  V  D  N  A  G  A  K  A  G  L  T  F

661     CTGGTTGACCTGATTAAAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAA
221      L  V  D  L  I  K  N  K  H  M  N  A  D  T  D  Y  S  I  A  E

721     GCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAAC
241      A  A  F  N  K  G  E  T  A  M  T  I  N  G  P  W  A  W  S  N

781     ATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCA
261      I  D  T  S  K  V  N  Y  G  V  T  V  L  P  T  F  K  G  Q  P

841     TCCAAACCGTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAG
281      S  K  P  F  V  G  V  L  S  A  G  I  N  A  A  S  P  N  K  E

901     CTGGCGAAAGAGTTCCTCGAAAACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAAT
301      L  A  K  E  F  L  E  N  Y  L  L  T  D  E  G  L  E  A  V  N

961     AAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGAT
321      K  D  K  P  L  G  A  V  A  L  K  S  Y  E  E  E  L  A  K  D
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1021  CCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATGCCGAACATCCCG
341    P  R  I  A  A  T  M  E  N  A  Q  K  G  E  I  M  P  N  I  P

                                          Factor Xa   +43 NTR
1081  CAGATGTCCGCTTTCTGGTATGCCGTGCTGATCGAAGCCCGCACCTCGGAATCCGACACG
361    Q  M  S  A  F  W  Y  A  V  L  I  E  A  R  T  S  E  S  D  T

1141  GCAGGGCCCAACAGCGACCTGGACGTGAACACTGACATTTATTCCAAGGTGCTGGTGACT
381    A  G  P  N  S  D  L  D  V  N  T  D  I  Y  S  K  V  L  V  T

1201  GCTATATACCTGGCACTCTTCGTGGTGGGCACTGTGGGCAACTCCGTGACAGCCTTCACT
401    A  I  Y  L  A  L  F  V  V  G  T  V  G  N  S  V  T  A  F  T

1261  CTAGCGCGGAAGAAGTCACTGCAGAGCCTGCAGAGCACTGTGCATTACCACCTGGGCAGC
421    L  A  R  K  K  S  L  Q  S  L  Q  S  T  V  H  Y  H  L  G  S

1321  CTGGCACTGTCGGACCTGCTTATCCTTCTGCTGGCCATGCCCGTGGAGCTATACAACTTC
441    L  A  L  S  D  L  L  I  L  L  L  A  M  P  V  E  L  Y  N  F

1381  ATCTGGGTACACCATCCCTGGGCCTTTGGGGACGCTGGCTGCCGTGGCTACTATTTCCTG
461    I  W  V  H  H  P  W  A  F  G  D  A  G  C  R  G  Y  Y  F  L

1441  CGTGATGCCTGCACCTATGCCACAGCCCTCAATGTAGCCAGCCTGAGTGTGGAGCGCTAC
481    R  D  A  C  T  Y  A  T  A  L  N  V  A  S  L  S  V  E  R  Y

1501  TTGGCCATCTGCCATCCCTTCAAGGCCAAGACCCTCATGTCCCGCAGCCGCACCAAGAAA
501    L  A  I  C  H  P  F  K  A  K  T  L  M  S  R  S  R  T  K  K

1561  TTCATCAGTGCCATATGGCTAGCTTCGGCGCTGCTGGCTATACCCATGCTTTTCACCATG
521    F  I  S  A  I  W  L  A  S  A  L  L  A  I  P  M  L  F  T  M

1621  GGCCTGCAGAACCGCAGTGGTGACGGCACGCACCCTGGCGGCCTGGTGTGCACACCCATT
541    G  L  Q  N  R  S  G  D  G  T  H  P  G  G  L  V  C  T  P  I

1681  GTGGACACAGCCACTGTCAAGGTCGTCATCCAGGTTAACACCTTCATGTCCTTCCTGTTT
561    V  D  T  A  T  V  K  V  V  I  Q  V  N  T  F  M  S  F  L  F

1741  CCCATGTTGGTCATCTCCATCCTAAACACCGTGATTGCCAACAAACTGACAGTCATGGTG
581    P  M  L  V  I  S  I  L  N  T  V  I  A  N  K  L  T  V  M  V

1801  CACCAGGCCGCCGAGCAGGGCCGAGTGTGCACCGTGGGCACACACAACGGTTTAGAGCAC
601    H  Q  A  A  E  Q  G  R  V  C  T  V  G  T  H  N  G  L  E  H

1861  AGCACGTTCAACATGACCATCGAGCCGGGTCGTGTCCAGGCCCTGCGCCACGGAGTCCTC
621    S  T  F  N  M  T  I  E  P  G  R  V  Q  A  L  R  H  G  V  L

1921  GTCTTACGTGCTGTGGTCATTGCCTTTGTGGTCTGCTGGCTGCCCTACCACGTGCGACGC
641    V  L  R  A  V  V  I  A  F  V  V  C  W  L  P  Y  H  V  R  R

1981  CTGATGTTCTGCTATATCTCGGATGAACAGTGGACTACGTTCCTCTTCGATTTCTACCAC
661    L  M  F  C  Y  I  S  D  E  Q  W  T  T  F  L  F  D  F  Y  H

2041  TATTTCTACATGCTAACCAACGCTCTCTTCTACGTCAGCTCCGCCATCAATCCCATCCTC
681    Y  F  Y  M  L  T  N  A  L  F  Y  V  S  S  A  I  N  P  I  L

2101  TACAACCTGGTCTCCGCCAACTTCCGCCAGGTCTTTCTGTCCACGCTGGCCTGCCTTTGT
701    Y  N  L  V  S  A  N  F  R  Q  V  F  L  S  T  L  A  C  L  C

2161  CCTGGGTGGCGCCACCGCCGAAAGAAGAGGCCAACGTTCTCCAGGAAGCCCAACAGCATG
721    P  G  W  R  H  R  R  K  K  R  P  T  F  S  R  K  P  N  S  M
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```
                                                                  NotI
2221    TCCAGCAACCATGCCTTTTCCACCAGCGCCACCCGGGAGACCCTGTACgcggccgca
741      S  S  N  H  A  F  S  T  S  A  T  R  E  T  L  Y  A  A  A

              Flag              stop  KpnI
GATTATAAAGATGACGATGACAAATAATAAGGTACC
 D  Y  K  D  D  D  D  K  *  *
```

SEQ ID NO.: 167

MalE (1-28) Factor Xa NTR (43-424) FLAG

```
     SalI  +1 MalE leader (1-28)
1    gtcgacATGAAAATAAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTT
1          M  K  I  K  T  G  A  R  I  L  A  L  S  A  L  T  T  M  M  F

                                        Factor Xa  +43 NTR
61       TCCGCCTCGGCTCTCGCCAAAATCATCGAAGCCCGCACCTCGGAATCCGACACGGCAGGG
21        S  A  S  A  L  A  K  I  I  E  A  R  T  S  E  S  D  T  A  G

121      CCCAACAGCGACCTGGACGTGAACACTGACATTTATTCCAAGGTGCTGGTGACTGCTATA
41        P  N  S  D  L  D  V  N  T  D  I  Y  S  K  V  L  V  T  A  I

181      TACCTGGCACTCTTCGTGGTGGGCACTGTGGGCAACTCCGTGACAGCCTTCACTCTAGCG
61        Y  L  A  L  F  V  V  G  T  V  G  N  S  V  T  A  F  T  L  A

241      CGGAAGAAGTCACTGCAGAGCCTGCAGAGCACTGTGCATTACCACCTGGGCAGCCTGGCA
81        R  K  K  S  L  Q  S  L  Q  S  T  V  H  Y  H  L  G  S  L  A

301      CTGTCGGACCTGCTTATCCTTCTGCTGGCCATGCCCGTGGAGCTATACAACTTCATCTGG
101       L  S  D  L  L  I  L  L  L  A  M  P  V  E  L  Y  N  F  I  W

361      GTACACCATCCCTGGGCCTTTGGGGACGCTGGCTGCCGTGGCTACTATTTCCTGCGTGAT
121       V  H  H  P  W  A  F  G  D  A  G  C  R  G  Y  Y  F  L  R  D

421      GCCTGCACCTATGCCACAGCCCTCAATGTAGCCAGCCTGAGTGTGGAGCGCTACTTGGCC
141       A  C  T  Y  A  T  A  L  N  V  A  S  L  S  V  E  R  Y  L  A

481      ATCTGCCATCCCTTCAAGGCCAAGACCCTCATGTCCCGCAGCCGCACCAAGAAATTCATC
161       I  C  H  P  F  K  A  K  T  L  M  S  R  S  R  T  K  K  F  I

541      AGTGCCATATGGCTAGCTTCGGCGCTGCTGGCTATACCCATGCTTTTCACCATGGGCCTG
181       S  A  I  W  L  A  S  A  L  L  A  I  P  M  L  F  T  M  G  L

601      CAGAACCGCAGTGGTGACGGCACGCACCCTGGCGGCCTGGTGTGCACACCCATTGTGGAC
201       Q  N  R  S  G  D  G  T  H  P  G  G  L  V  C  T  P  I  V  D

661      ACAGCCACTGTCAAGGTCGTCATCCAGGTTAACACCTTCATGTCCTTCCTGTTTCCCATG
221       T  A  T  V  K  V  V  I  Q  V  N  T  F  M  S  F  L  F  P  M

721      TTGGTCATCTCCATCCTAAACACCGTGATTGCCAACAAACTGACAGTCATGGTGCACCAG
241       L  V  I  S  I  L  N  T  V  I  A  N  K  L  T  V  M  V  H  Q

781      GCCGCCGAGCAGGGCCGAGTGTGCACCGTGGGCACACACAACGGTTTAGAGCACAGCACG
261       A  A  E  Q  G  R  V  C  T  V  G  T  H  N  G  L  E  H  S  T
```

```
841        TTCAACATGACCATCGAGCCGGGTCGTGTCCAGGCCCTGCGCCACGGAGTCCTCGTCTTA
281         F  N  M  T  I  E  P  G  R  V  Q  A  L  R  H  G  V  L  V  L

901        CGTGCTGTGGTCATTGCCTTTGTGGTCTGCTGGCTGCCCTACCACGTGCGACGCCTGATG
301         R  A  V  V  I  A  F  V  V  C  W  L  P  Y  H  V  R  R  L  M

961        TTCTGCTATATCTCGGATGAACAGTGGACTACGTTCCTCTTCGATTTCTACCACTATTTC
321         F  C  Y  I  S  D  E  Q  W  T  T  F  L  F  D  F  Y  H  Y  F

1021       TACATGCTAACCAACGCTCTCTTCTACGTCAGCTCCGCCATCAATCCCATCCTCTACAAC
341         Y  M  L  T  N  A  L  F  Y  V  S  S  A  I  N  P  I  L  Y  N

1081       CTGGTCTCCGCCAACTTCCGCCAGGTCTTTCTGTCCACGCTGGCCTGCCTTTGTCCTGGG
361         L  V  S  A  N  F  R  Q  V  F  L  S  T  L  A  C  L  C  P  G

1141       TGGCGCCACCGCCGAAAGAAGAGGCCAACGTTCTCCAGGAAGCCCAACAGCATGTCCAGC
381         W  R  H  R  R  K  K  R  P  T  F  S  R  K  P  N  S  M  S  S

                                                          NotI      Flag
1201       AACCATGCCTTTTCCACCAGCGCCACCCGGGAGACCCTGTACgcggccgcaGATTATAAA
401         N  H  A  F  S  T  S  A  T  R  E  T  L  Y  A  A  A  D  Y  K

                          stop  KpnI
           GATGACGATGACAAATAATAAGGTACC
                D  D  D  D  K
```

SEQ ID NO.: 169

MalE (1-370) Factor Xa NTR (43-424) TrxA (2-109) FLAG

```
      SalI +1 MalE (1-370)
1    GTCGACATGAAAATAAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTT
1           M  K  I  K  T  G  A  R  I  L  A  L  S  A  L  T  T  M  M  F

61         TCCGCCTCGGCTCTCGCCAAAATCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGAT
21          S  A  S  A  L  A  K  I  E  E  G  K  L  V  I  W  I  N  G  D

121        AAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAA
41          K  G  Y  N  G  L  A  E  V  G  K  K  F  E  K  D  T  G  I  K

181        GTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGC
61          V  T  V  E  H  P  D  K  L  E  E  K  F  P  Q  V  A  A  T  G

241        GATGGCCCTGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGC
81          D  G  P  D  I  I  F  W  A  H  D  R  F  G  G  Y  A  Q  S  G

301        CTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGG
101         L  L  A  E  I  T  P  D  K  A  F  Q  D  K  L  Y  P  F  T  W

361        GATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCG
121         D  A  V  R  Y  N  G  K  L  I  A  Y  P  I  A  V  E  A  L  S

421        CTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCG
141         L  I  Y  N  K  D  L  L  P  N  P  P  K  T  W  E  E  I  P  A

481        CTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCG
161         L  D  K  E  L  K  A  K  G  K  S  A  L  M  F  N  L  Q  E  P
```

```
      541  TACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGC
      181   Y  F  T  W  P  L  I  A  A  D  G  G  Y  A  F  K  Y  E  N  G

      601  AAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTC
      201   K  Y  D  I  K  D  V  G  V  D  N  A  G  A  K  A  G  L  T  F

      661  CTGGTTGACCTGATTAAAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAA
      221   L  V  D  L  I  K  N  K  H  M  N  A  D  T  D  Y  S  I  A  E

      721  GCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAAC
      241   A  A  F  N  K  G  E  T  A  M  T  I  N  G  P  W  A  W  S  N

      781  ATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCA
      261   I  D  T  S  K  V  N  Y  G  V  T  V  L  P  T  F  K  G  Q  P

      841  TCCAAACCGTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAG
      281   S  K  P  F  V  G  V  L  S  A  G  I  N  A  A  S  P  N  K  E

      901  CTGGCGAAAGAGTTCCTCGAAAACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAAT
      301   L  A  K  E  F  L  E  N  Y  L  L  T  D  E  G  L  E  A  V  N

      961  AAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGAT
      321   K  D  K  P  L  G  A  V  A  L  K  S  Y  E  E  E  L  A  K  D

     1021  CCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATGCCGAACATCCCG
      341   P  R  I  A  A  T  M  E  N  A  Q  K  G  E  I  M  P  N  I  P

                                                  Factor Xa   +43 NTR
     1081  CAGATGTCCGCTTTCTGGTATGCCGTGCTGATCGAAGCCCGCACCTCGGAATCCGACACG
      361   Q  M  S  A  F  W  Y  A  V  L  I  E  A  R  T  S  E  S  D  T

     1141  GCAGGGCCCAACAGCGACCTGGACGTGAACACTGACATTTATTCCAAGGTGCTGGTGACT
      381   A  G  P  N  S  D  L  D  V  N  T  D  I  Y  S  K  V  L  V  T

     1201  GCTATATACCTGGCACTCTTCGTGGTGGGCACTGTGGGCAACTCCGTGACAGCCTTCACT
      401   A  I  Y  L  A  L  F  V  V  G  T  V  G  N  S  V  T  A  F  T

     1261  CTAGCGCGGAAGAAGTCACTGCAGAGCCTGCAGAGCACTGTGCATTACCACCTGGGCAGC
      421   L  A  R  K  K  S  L  Q  S  L  Q  S  T  V  H  Y  H  L  G  S

     1321  CTGGCACTGTCGGACCTGCTTATCCTTCTGCTGGCCATGCCCGTGGAGCTATACAACTTC
      441   L  A  L  S  D  L  L  I  L  L  L  A  M  P  V  E  L  Y  N  F

     1381  ATCTGGGTACACCATCCCTGGGCCTTTGGGGACGCTGGCTGCCGTGGCTACTATTTCCTG
      461   I  W  V  H  H  P  W  A  F  G  D  A  G  C  R  G  Y  Y  F  L

     1441  CGTGATGCCTGCACCTATGCCACAGCCCTCAATGTAGCCAGCCTGAGTGTGGAGCGCTAC
      481   R  D  A  C  T  Y  A  T  A  L  N  V  A  S  L  S  V  E  R  Y

     1501  TTGGCCATCTGCCATCCCTTCAAGGCCAAGACCCTCATGTCCCGCAGCCGCACCAAGAAA
      501   L  A  I  C  H  P  F  K  A  K  T  L  M  S  R  S  R  T  K  K

     1561  TTCATCAGTGCCATATGGCTAGCTTCGGCGCTGCTGGCTATACCCATGCTTTTCACCATG
      521   F  I  S  A  I  W  L  A  S  A  L  L  A  I  P  M  L  F  T  M

     1621  GGCCTGCAGAACCGCAGTGGTGACGGCACGCACCCTGGCGGCCTGGTGTGCACACCCATT
      541   G  L  Q  N  R  S  G  D  G  T  H  P  G  G  L  V  C  T  P  I

     1681  GTGGACACAGCCACTGTCAAGGTCGTCATCCAGGTTAACACCTTCATGTCCTTCCTGTTT
      561   V  D  T  A  T  V  K  V  V  I  Q  V  N  T  F  M  S  F  L  F
```

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1741    CCCATGTTGGTCATCTCCATCCTAAACACCGTGATTGCCAACAAACTGACAGTCATGGTG
581      P  M  L  V  I  S  I  L  N  T  V  I  A  N  K  L  T  V  M  V

1801    CACCAGGCCGCCGAGCAGGGCCGAGTGTGCACCGTGGGCACACACAACGGTTTAGAGCAC
601      H  Q  A  A  E  Q  G  R  V  C  T  V  G  T  H  N  G  L  E  H

1861    AGCACGTTCAACATGACCATCGAGCCGGGTCGTGTCCAGGCCCTGCGCCACGGAGTCCTC
621      S  T  F  N  M  T  I  E  P  G  R  V  Q  A  L  R  H  G  V  L

1921    GTCTTACGTGCTGTGGTCATTGCCTTTGTGGTCTGCTGGCTGCCCTACCACGTGCGACGC
641      V  L  R  A  V  V  I  A  F  V  V  C  W  L  P  Y  H  V  R  R

1981    CTGATGTTCTGCTATATCTCGGATGAACAGTGGACTACGTTCCTCTTCGATTTCTACCAC
661      L  M  F  C  Y  I  S  D  E  Q  W  T  T  F  L  F  D  F  Y  H

2041    TATTTCTACATGCTAACCAACGCTCTCTTCTACGTCAGCTCCGCCATCAATCCCATCCTC
681      Y  F  Y  M  L  T  N  A  L  F  Y  V  S  S  A  I  N  P  I  L

2101    TACAACCTGGTCTCCGCCAACTTCCGCCAGGTCTTTCTGTCCACGCTGGCCTGCCTTTGT
701      Y  N  L  V  S  A  N  F  R  Q  V  F  L  S  T  L  A  C  L  C

2161    CCTGGGTGGCGCCACCGCCGAAAGAAGAGGCCAACGTTCTCCAGGAAGCCCAACAGCATG
721      P  G  W  R  H  R  R  K  K  R  P  T  F  S  R  K  P  N  S  M

                                                          NotI   +2
                                        TrxA
2221    TCCAGCAACCATGCCTTTTCCACCAGCGCCACCCGGGAGACCCTGTACgcggccgcaAGC
741      S  S  N  H  A  F  S  T  S  A  T  R  E  T  L  Y  A  A  A  S

2281    GATAAAATTATTCACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGG
761      D  K  I  I  H  L  T  D  D  S  F  D  T  D  V  L  K  A  D  G

2341    GCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATT
781      A  I  L  V  D  F  W  A  E  W  C  G  P  C  K  M  I  A  P  I

2401    CTGGATGAAATCGCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAACATCGAT
801      L  D  E  I  A  D  E  Y  Q  G  K  L  T  V  A  K  L  N  I  D

2461    CAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTC
821      Q  N  P  G  T  A  P  K  Y  G  I  R  G  I  P  T  L  L  L  F

2521    AAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAG
841      K  N  G  E  V  A  A  T  K  V  G  A  L  S  K  G  Q  L  K  E

                                  NotI   +2 Flag                stop
2581    TTCCTCGACGCTAACCTGGCGgcggccgcaGATTATAAAGATGACGATGACAAATAATAA
861      F  L  D  A  N  L  A  A  A  A  D  Y  K  D  D  D  D  K  *  *

         KpnI
2641    GGTACC
```

SEQ ID NO.: 170

MalE (1-28) Factor Xa NTR (43-424) TrxA (2-109) FLAG

SalI +1 MalE leader (1-28)

```
1    gtcgacATGAAAATAAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTT
1          M  K  I  K  T  G  A  R  I  L  A  L  S  A  L  T  T  M  M  F

                                        Factor Xa  +43 NTR
61         TCCGCCTCGGCTCTCGCCAAAATCATCGAAGCCCGCACCTCGGAATCCGACACGGCAGGG
21          S  A  S  A  L  A  K  I  I  E  A  R  T  S  E  S  D  T  A  G

121        CCCAACAGCGACCTGGACGTGAACACTGACATTTATTCCAAGGTGCTGGTGACTGCTATA
41          P  N  S  D  L  D  V  N  T  D  I  Y  S  K  V  L  V  T  A  I

181        TACCTGGCACTCTTCGTGGTGGGCACTGTGGGCAACTCCGTGACAGCCTTCACTCTAGCG
61          Y  L  A  L  F  V  V  G  T  V  G  N  S  V  T  A  F  T  L  A

241        CGGAAGAAGTCACTGCAGAGCCTGCAGAGCACTGTGCATTACCACCTGGGCAGCCTGGCA
81          R  K  K  S  L  Q  S  L  Q  S  T  V  H  Y  H  L  G  S  L  A

301        CTGTCGGACCTGCTTATCCTTCTGCTGGCCATGCCCGTGGAGCTATACAACTTCATCTGG
101         L  S  D  L  L  I  L  L  L  A  M  P  V  E  L  Y  N  F  I  W

361        GTACACCATCCCTGGGCCTTTGGGGACGCTGGCTGCCGTGGCTACTATTTCCTGCGTGAT
121         V  H  H  P  W  A  F  G  D  A  G  C  R  G  Y  Y  F  L  R  D

421        GCCTGCACCTATGCCACAGCCCTCAATGTAGCCAGCCTGAGTGTGGAGCGCTACTTGGCC
141         A  C  T  Y  A  T  A  L  N  V  A  S  L  S  V  E  R  Y  L  A

481        ATCTGCCATCCCTTCAAGGCCAAGACCCTCATGTCCCGCAGCCGCACCAAGAAATTCATC
161         I  C  H  P  F  K  A  K  T  L  M  S  R  S  R  T  K  K  F  I

541        AGTGCCATATGGCTAGCTTCGGCGCTGCTGGCTATACCCATGCTTTTCACCATGGGCCTG
181         S  A  I  W  L  A  S  A  L  L  A  I  P  M  L  F  T  M  G  L

601        CAGAACCGCAGTGGTGACGGCACGCACCCTGGCGGCCTGGTGTGCACACCCATTGTGGAC
201         Q  N  R  S  G  D  G  T  H  P  G  G  L  V  C  T  P  I  V  D

661        ACAGCCACTGTCAAGGTCGTCATCCAGGTTAACACCTTCATGTCCTTCCTGTTTCCCATG
221         T  A  T  V  K  V  V  I  Q  V  N  T  F  M  S  F  L  F  P  M

721        TTGGTCATCTCCATCCTAAACACCGTGATTGCCAACAAACTGACAGTCATGGTGCACCAG
241         L  V  I  S  I  L  N  T  V  I  A  N  K  L  T  V  M  V  H  Q

781        GCCGCCGAGCAGGGCCGAGTGTGCACCGTGGGCACACACAACGGTTTAGAGCACAGCACG
261         A  A  E  Q  G  R  V  C  T  V  G  T  H  N  G  L  E  H  S  T

841        TTCAACATGACCATCGAGCCGGGTCGTGTCCAGGCCCTGCGCCACGGAGTCCTCGTCTTA
281         F  N  M  T  I  E  P  G  R  V  Q  A  L  R  H  G  V  L  V  L

901        CGTGCTGTGGTCATTGCCTTTGTGGTCTGCTGGCTGCCCTACCACGTGCGACGCCTGATG
301         R  A  V  V  I  A  F  V  V  C  W  L  P  Y  H  V  R  R  L  M

961        TTCTGCTATATCTCGGATGAACAGTGGACTACGTTCCTCTTCGATTTCTACCACTATTTC
321         F  C  Y  I  S  D  E  Q  W  T  T  F  L  F  D  F  Y  H  Y  F

1021       TACATGCTAACCAACGCTCTCTTCTACGTCAGCTCCGCCATCAATCCCATCCTCTACAAC
341         Y  M  L  T  N  A  L  F  Y  V  S  S  A  I  N  P  I  L  Y  N

1081       CTGGTCTCCGCCAACTTCCGCCAGGTCTTTCTGTCCACGCTGGCCTGCCTTTGTCCTGGG
361         L  V  S  A  N  F  R  Q  V  F  L  S  T  L  A  C  L  C  P  G

1141       TGGCGCCACCGCCGAAAGAAGAGGCCAACGTTCTCCAGGAAGCCCAACAGCATGTCCAGC
```

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381        W  R  H  R  R  K  K  R  P  T  F  S  R  K  P  N  S  M  S  S

                                                        NotI   +2 TrxA
1201       AACCATGCCTTTTCCACCAGCGCCACCCGGGAGACCCTGTACgcggccgcaAGCGATAAA
401         N  H  A  F  S  T  S  A  T  R  E  T  L  Y  A  A  A  S  D  K

1261       ATTATTCACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATC
421         I  I  H  L  T  D  D  S  F  D  T  D  V  L  K  A  D  G  A  I

1321       CTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGAT
441         L  V  D  F  W  A  E  W  C  G  P  C  K  M  I  A  P  I  L  D

1381       GAAATCGCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAACATCGATCAAAAC
461         E  I  A  D  E  Y  Q  G  K  L  T  V  A  K  L  N  I  D  Q  N

1441       CCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAAC
481         P  G  T  A  P  K  Y  G  I  R  G  I  P  T  L  L  L  F  K  N

1501       GGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGTTCCTC
501         G  E  V  A  A  T  K  V  G  A  L  S  K  G  Q  L  K  E  F  L

                              NotI              Flag              stop  KpnI
1561       GACGCTAACCTGGCAgcggccgcaGATTATAAAGATGACGATGACAAATAATAAGGTACC
521         D  A  N  L  A  A  A  A  D  Y  K  D  D  D  D  K
```

SEQ ID NO.: 188

Human β2AR GS1α chimeric fusion

```
          SalI  +1 B2AR
1       GTCGACATGG GGCAACCCGG GAACGGCAGC GCCTTCTTGC TGGCACCCAA
TGGAAGCCAT

61      GCGCCGGACC ACGACGTCAC GCAGCAAAGG GACGAGGTGT GGGTGGTGGG
CATGGGCATC
121     GTCATGTCTC TCATCGTCCT GGCCATCGTG TTTGGCAATG TGCTGGTCAT
CACAGCCATT
181     GCCAAGTTCG AGCGTCTGCA GACGGTCACC AACTACTTCA TCACTTCACT
GGCCTGTGCT
241     GATCTGGTCA TGGGCCTAGC AGTGGTGCCC TTTGGGGCCG CCCATATTCT
TATGAAAATG
301     TGGACTTTTG GCAACTTCTG GTGCGAGTTT TGGACTTCCA TTGATGTGCT
GTGCGTCACG
361     GCCAGCATTG AGACCCTGTG CGTGATCGCA GTGGATCGCT ACTTTGCCAT
TACTTCACCT
421     TTCAAGTACC AGAGCCTGCT GACCAAGAAT AAGGCCCGGG TGATCATTCT
GATGGTGTGG
481     ATTGTGTCAG GCCTTAYCTC CTTCTTGCCC ATTCAGATGC ACTGGTACAG
GGCCACCCAC
541     CAGGAAGCCA TCAACTGCTA TGCCAATGAG ACCTGCTGTG ACTTCTTCAC
GAACCAAGCC
601     TATGCCATTG CCTCTTCCAT CGTGTCCTTC TACGTTCCCC TGGTGATCAT
GGTCTTCGTC
661     TACTCCAGGG TCTTTCAGGA GGCCAAAAGG CAGCTCCAGA AGATTGACAA
ATCTGAGGGC
721     CGCTTCCATG TCCAGAACCT TAGCCAGGTG GAGCAGGATG GGCGGACGGG
GCATGGACTC
```

781 CGCAGATCTT CCAAGTTCTG CTTGAAGGAG CACAAAGCCC TCAAGACGTT
AGGCATCATC
841 ATGGGCACTT TCACCCTCTG CTGGCTGCCC TTCTTCATCG TTAACATTGT
GCATGTGATC
901 CAGGATAACC TCATCCGTAA GGAAGTTTAC ATCCTCCTAA ATTGGATAGG
CTATGTCAAT
961 TCTGGTTTCA ATCCCCTTAT CTACTGCCGG AGCCCAGATT TCAGGATTGC
CTTCCAGGAG
1021 CTTCTGTGCC TGCGCAGGTC TTCTTTGAAG GCCTATGGCA ATGGCTACTC
CAGCAACGGC
1081 AACACAGGGG AGCAGAGTGG ATATCACGTG GAACAGGAGA AAGAAAATAA
ACTGCTGTGT
1141 GAAGACCTCC CAGGCACGGA AGACTTTGTG GGCCATCAAG GTACTGTGCC
TAGCGATAAC

Last B2AR Linker sequence

1201 ATTGATTCAC AAGGGAGGAA TTGTAGTACA AATGACTCAC TGCTA**GAGCG**
TGGCCAGACG

PstI XhoI +2 GS1 alpha

1261 GTCACCAACC TGCAG**CTCGA GGGC**TGCCTC GGGAACAGTA AGACCGAGGA
CCAGCGCAAC

1321 GAGGAGAAGG CGCAGCGTGA GGCCAACAAA AAGATCGAGA AGCAGCTGCA
GAAGGACAAG
1381 CAGGTCTACC GGGCCACGCA CCGCCTGCTG CTGCTGGGTG CTGGAGAATC
TGGTAAAAGC
1441 ACCATTGTGA AGCAGATGAG GATCCTGCAT GTTAATGGGT TTAATGGAGA
CAGTGAGAAG
1501 GCAACCAAAG TGCAGGACAT CAAAAACAAC CTGAAAGAGG CGATTGAAAC
CATTGTGGCC
1561 GCCATGAGCA ACCTGGTGCC CCCCGTGGAG CTGGCCAACC CCGAGAACCA
GTTCAGAGTG
1621 GACTACATCC TGAGTGTGAT GAACGTGCCT GACTTTGACT TCCCTCCCGA
ATTCTATGAG
1681 CATGCCAAGG CTCTGTGGGA GGATGAAGGA GTGCGTGCCT GCTACGAACG
CTCCAACGAG
1741 TACCAGCTGA TTGACTGTGC CCAGTACTTC CTGGACAAGA TCGACGTGAT
CAAGCAGGCT
1801 GACTATGTGC CGAGCGATCA GGACCTGCTT CGCTGCCGTG TCCTGACTTC
TGGAATCTTT
1861 GAGACCAAGT TCCAGGTGGA CAAAGTCAAC TTCCACATGT TTGACGTGGG
TGGCCAGCGC
1921 GATGAACGCC GCAAGTGGAT CCAGTGCTTC AACGATGTGA CTGCCATCAT
CTTCGTGGTG
1981 GCCAGCAGCA GCTACAACAT GGTCATCCGG GAGGACAACC AGACCAACCG
CCTGCAGGAG
2041 GCTCTGAACC TCTTCAAGAG CATCTGGAAC AACAGATGGC TGCGCACCAT
CTCTGTGATC
2101 CTGTTCCTCA ACAAGCAAGA TCTGCTCGCT GAGAAAGTCC TTGCTGGGAA
ATCGAAGATT
2161 GAGGACTACT TTCCAGAATT TGCTCGCTAC ACTACTCCTG AGGATGCTAC
TCCCGAGCCC
2221 GGAGAGGACC CACGCGTGAC CCGGGCCAAG TACTTCATTC GAGATGAGTT
TCTGAGGATC
2281 AGCACTGCCA GTGGAGATGG GCGTCACTAC TGCTACCCTC ATTTCACCTG
CGCTGTGGAC

2341 ACTGAGAACA TCCGCCGTGT GTTCAACGAC TGCCGTGACA TCATTCAGCG
CATGCACCTT

ClaI Stop XbaI Stem-loop
2401 CGTCAGTACG AGCTGCTCAT CGATTAATAA TCTAGAGGAT CCCCGCGCCC
TCATCCGAAA

2461 GGGCG

SEQ ID NO.: 190

Human β2AR stop GS1α transcriptional fusion

PstI +1 B2AR
1 GTCGACATGG GGCAACCCGG GAACGGCAGC GCCTTCTTGC TGGCACCCAA
TGGAAGCCAT

61 GCGCCGGACC ACGACGTCAC GCAGCAAAGG GACGAGGTGT GGGTGGTGGG
CATGGGCATC
121 GTCATGTCTC TCATCGTCCT GGCCATCGTG TTTGGCAATG TGCTGGTCAT
CACAGCCATT
181 GCCAAGTTCG AGCGTCTGCA GACGGTCACC AACTACTTCA TCACTTCACT
GGCCTGTGCT
241 GATCTGGTCA TGGGCCTAGC AGTGGTGCCC TTTGGGGCCG CCCATATTCT
TATGAAAATG
301 TGGACTTTTG GCAACTTCTG GTGCGAGTTT TGGACTTCCA TTGATGTGCT
GTGCGTCACG
361 GCCAGCATTG AGACCCTGTG CGTGATCGCA GTGGATCGCT ACTTTGCCAT
TACTTCACCT
421 TTCAAGTACC AGAGCCTGCT GACCAAGAAT AAGGCCCGGG TGATCATTCT
GATGGTGTGG
481 ATTGTGTCAG GCCTTAYCTC CTTCTTGCCC ATTCAGATGC ACTGGTACAG
GGCCACCCAC
541 CAGGAAGCCA TCAACTGCTA TGCCAATGAG ACCTGCTGTG ACTTCTTCAC
GAACCAAGCC
601 TATGCCATTG CCTCTTCCAT CGTGTCCTTC TACGTTCCCC TGGTGATCAT
GGTCTTCGTC
661 TACTCCAGGG TCTTTCAGGA GGCCAAAAGG CAGCTCCAGA AGATTGACAA
ATCTGAGGGC
721 CGCTTCCATG TCCAGAACCT TAGCCAGGTG GAGCAGGATG GGCGGACGGG
GCATGGACTC
781 CGCAGATCTT CCAAGTTCTG CTTGAAGGAG CACAAAGCCC TCAAGACGTT
AGGCATCATC
841 ATGGGCACTT TCACCCTCTG CTGGCTGCCC TTCTTCATCG TTAACATTGT
GCATGTGATC
901 CAGGATAACC TCATCCGTAA GGAAGTTTAC ATCCTCCTAA ATTGGATAGG
CTATGTCAAT
961 TCTGGTTTCA ATCCCCTTAT CTACTGCCGG AGCCCAGATT TCAGGATTGC
CTTCCAGGAG
1021 CTTCTGTGCC TGCGCAGGTC TTCTTTGAAG GCCTATGGCA ATGGCTACTC
CAGCAACGGC
1081 AACACAGGGG AGCAGAGTGG ATATCACGTG GAACAGGAGA AAGAAAATAA
ACTGCTGTGT
1141 GAAGACCTCC CAGGCACGGA AGACTTTGTG GGCCATCAAG GTACTGTGCC
TAGCGATAAC

Last B2AR Linker sequence

1201 ATTGATTCAC AAGGGAGGAA TTGTAGTACA AATGACTCAC TGCTA**GAGCG TGGCCAGACG**

PstI Stop SD XhoI +2 GS1 alpha

1261 GTCACCAACC TGCAGTAATA ATCAAGGAGG CCCTCGAGAT GGGCTGCCTC GGGAACAGTA

1321 AGACCGAGGA CCAGCGCAAC GAGGAGAAGG CGCAGCGTGA GGCCAACAAA AAGATCGAGA

1381 AGCAGCTGCA GAAGGACAAG CAGGTCTACC GGGCCACGCA CCGCCTGCTG CTGCTGGGTG

1441 CTGGAGAATC TGGTAAAAGC ACCATTGTGA AGCAGATGAG GATCCTGCAT GTTAATGGGT

1501 TTAATGGAGA CAGTGAGAAG GCAACCAAAG TGCAGGACAT CAAAAACAAC CTGAAAGAGG

1561 CGATTGAAAC CATTGTGGCC GCCATGAGCA ACCTGGTGCC CCCCGTGGAG CTGGCCAACC

1621 CCGAGAACCA GTTCAGAGTG GACTACATCC TGAGTGTGAT GAACGTGCCT GACTTTGACT

1681 TCCCTCCCGA ATTCTATGAG CATGCCAAGG CTCTGTGGGA GGATGAAGGA GTGCGTGCCT

1741 GCTACGAACG CTCCAACGAG TACCAGCTGA TTGACTGTGC CCAGTACTTC CTGGACAAGA

1801 TCGACGTGAT CAAGCAGGCT GACTATGTGC CGAGCGATCA GGACCTGCTT CGCTGCCGTG

1861 TCCTGACTTC TGGAATCTTT GAGACCAAGT TCCAGGTGGA CAAAGTCAAC TTCCACATGT

1921 TTGACGTGGG TGGCCAGCGC GATGAACGCC GCAAGTGGAT CCAGTGCTTC AACGATGTGA

1981 CTGCCATCAT CTTCGTGGTG GCCAGCAGCA GCTACAACAT GGTCATCCGG GAGGACAACC

2041 AGACCAACCG CCTGCAGGAG GCTCTGAACC TCTTCAAGAG CATCTGGAAC AACAGATGGC

2101 TGCGCACCAT CTCTGTGATC CTGTTCCTCA ACAAGCAAGA TCTGCTCGCT GAGAAAGTCC

2161 TTGCTGGGAA ATCGAAGATT GAGGACTACT TTCCAGAATT TGCTCGCTAC ACTACTCCTG

2221 AGGATGCTAC TCCCGAGCCC GGAGAGGACC CACGCGTGAC CCGGGCCAAG TACTTCATTC

2281 GAGATGAGTT TCTGAGGATC AGCACTGCCA GTGGAGATGG GCGTCACTAC TGCTACCCTC

2341 ATTTCACCTG CGCTGTGGAC ACTGAGAACA TCCGCCGTGT GTTCAACGAC TGCCGTGACA

ClaI Stop XbaI

2401 TCATTCAGCG CATGCACCTT CGTCAGTACG AGCTGCTCAT CGAT**TAATAA** TCTAGAGGAT

Stem-loop

2461 CCCCGCGCCC TCATCCGAAA GGGCG

SEQ ID NO.: 192

Human GS1α

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          XhoI
          1
          CTCGAGATGGGCTGCCTCGGGAACAGTAAGACCGAGGACCAGCGCAACGAGGAGAAGGCGCAGCGT
1         1          M  G  C  L  G  N  S  K  T  E  D  Q  R  N  E  E  K  A  Q  R

          61        GAGGCCAACAAAAAGATCGAGAAGCAGCTGCAGAAGGACAAGCAGGTCTACCGGGCCACG
          21         E  A  N  K  K  I  E  K  Q  L  Q  K  D  K  Q  V  Y  R  A  T

          121       CACCGCCTGCTGCTGCTGGGTGCTGGAGAATCTGGTAAAAGCACCATTGTGAAGCAGATG
          41         H  R  L  L  L  L  G  A  G  E  S  G  K  S  T  I  V  K  Q  M

          181       AGGATCCTGCATGTTAATGGGTTTAATGGAGACAGTGAGAAGGCAACCAAAGTGCAGGAC
          61         R  I  L  H  V  N  G  F  N  G  D  S  E  K  A  T  K  V  Q  D

          241       ATCAAAAACAACCTGAAAGAGGCGATTGAAACCATTGTGGCCGCCATGAGCAACCTGGTG
          81         I  K  N  N  L  K  E  A  I  E  T  I  V  A  A  M  S  N  L  V

          301       CCCCCCGTGGAGCTGGCCAACCCCGAGAACCAGTTCAGAGTGGACTACATCCTGAGTGTG
100       101        P  P  V  E  L  A  N  P  E  N  Q  F  R  V  D  Y  I  L  S  V

          361       ATGAACGTGCCTGACTTTGACTTCCCTCCCGAATTCTATGAGCATGCCAAGGCTCTGTGG
          121        M  N  V  P  D  F  D  F  P  P  E  F  Y  E  H  A  K  A  L  W

          421       GAGGATGAAGGAGTGCGTGCCTGCTACGAACGCTCCAACGAGTACCAGCTGATTGACTGT
          141        E  D  E  G  V  R  A  C  Y  E  R  S  N  E  Y  Q  L  I  D  C

          481       GCCCAGTACTTCCTGGACAAGATCGACGTGATCAAGCAGGCTGACTATGTGCCGAGCGAT
          161        A  Q  Y  F  L  D  K  I  D  V  I  K  Q  A  D  Y  V  P  S  D

          541       CAGGACCTGCTTCGCTGCCGTGTCCTGACTTCTGGAATCTTTGAGACCAAGTTCCAGGTG
          181        Q  D  L  L  R  C  R  V  L  T  S  G  I  F  E  T  K  F  Q  V

          601       GACAAAGTCAACTTCCACATGTTTGACGTGGGTGGCCAGCGCGATGAACGCCGCAAGTGG
200       201        D  K  V  N  F  H  M  F  D  V  G  G  Q  R  D  E  R  R  K  W

          661       ATCCAGTGCTTCAACGATGTGACTGCCATCATCTTCGTGGTGGCCAGCAGCAGCTACAAC
          221        I  Q  C  F  N  D  V  T  A  I  I  F  V  V  A  S  S  S  Y  N

240       721       ATGGTCATCCGGGAGGACAACCAGACCAACCGCCTGCAGGAGGCTCTGAACCTCTTCAAG
          241        M  V  I  R  E  D  N  Q  T  N  R  L  Q  E  A  L  N  L  F  K

          781       AGCATCTGGAACAACAGATGGCTGCGCACCATCTCTGTGATCCTGTTCCTCAACAAGCAA
          261        S  I  W  N  N  R  W  L  R  T  I  S  V  I  L  F  L  N  K  Q

280       841       GATCTGCTCGCTGAGAAAGTCCTTGCTGGGAAATCGAAGATTGAGGACTACTTTCCAGAA
          281        D  L  L  A  E  K  V  L  A  G  K  S  K  I  E  D  Y  F  P  E

          901       TTTGCTCGCTACACTACTCCTGAGGATGCTACTCCCGAGCCCGGAGAGGACCCACGCGTG
300       301        F  A  R  Y  T  T  P  E  D  A  T  P  E  P  G  E  D  P  R  V

          961       ACCCGGGCCAAGTACTTCATTCGAGATGAGTTTCTGAGGATCAGCACTGCCAGTGGAGAT
          321        T  R  A  K  Y  F  I  R  D  E  F  L  R  I  S  T  A  S  G  D

340       1021      GGGCGTCACTACTGCTACCCTCATTTCACCTGCGCTGTGGACACTGAGAACATCCGCCGT
          341        G  R  H  Y  C  Y  P  H  F  T  C  A  V  D  T  E  N  I  R  R

          1081      GTGTTCAACGACTGCCGTGACATCATTCAGCGCATGCACCTTCGTCAGTACGAGCTGCTC
          361        V  F  N  D  C  R  D  I  I  Q  R  M  H  L  R  Q  Y  E  L  L
360
```

ClaI
ATCGAT

SEQ ID NO.: 193

Human GS2α

XhoI

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1   CTCGAGATGGGCTGCCTCGGGAACAGTAAGACCGAGGACCAGCGCAACGAGGAGAAGGCGCAGCGT
1          M  G  C  L  G  N  S  K  T  E  D  Q  R  N  E  E  K  A  Q  R

61         GAGGCCAACAAAAAGATCGAGAAGCAGCTGCAGAAGGACAAGCAGGTCTACCGGGCCACG
21          E  A  N  K  K  I  E  K  Q  L  Q  K  D  K  Q  V  Y  R  A  T

121        CACCGCCTGCTGCTGCTGGGTGCTGGAGAATCTGGTAAAAGCACCATTGTGAAGCAGATG
41          H  R  L  L  L  L  G  A  G  E  S  G  K  S  T  I  V  K  Q  M

181        AGGATCCTGCATGTTAATGGGTTTAATGGAGAGGGCGGCGAAGAGGACCCGCAGGCTGCA
61          R  I  L  H  V  N  G  F  N  G  E  G  G  E  E  D  P  Q  A  A

241        AGGAGCAACAGCGATGGTGAGAAGGCAACCAAAGTGCAGGACATCAAAAACAACCTGAAA
81          R  S  N  S  D  G  E  K  A  T  K  V  Q  D  I  K  N  N  L  K

301        GAGGCGATTGAAACCATTGTGGCCGCCATGAGCAACCTGGTGCCCCCCGTGGAGCTGGCC
101         E  A  I  E  T  I  V  A  A  M  S  N  L  V  P  P  V  E  L  A

361        AACCCCGAGAACCAGTTCAGAGTGGACTACATCCTGAGTGTGATGAACGTGCCTGACTTT
121         N  P  E  N  Q  F  R  V  D  Y  I  L  S  V  M  N  V  P  D  F

421        GACTTCCCTCCCGAATTCTATGAGCATGCCAAGGCTCTGTGGGAGGATGAAGGAGTGCGT
141         D  F  P  P  E  F  Y  E  H  A  K  A  L  W  E  D  E  G  V  R

481        GCCTGCTACGAACGCTCCAACGAGTACCAGCTGATTGACTGTGCCCAGTACTTCCTGGAC
161         A  C  Y  E  R  S  N  E  Y  Q  L  I  D  C  A  Q  Y  F  L  D

541        AAGATCGACGTGATCAAGCAGGCTGACTATGTGCCGAGCGATCAGGACCTGCTTCGCTGC
181         K  I  D  V  I  K  Q  A  D  Y  V  P  S  D  Q  D  L  L  R  C

601        CGTGTCCTGACTTCTGGAATCTTTGAGACCAAGTTCCAGGTGGACAAAGTCAACTTCCAC
201         R  V  L  T  S  G  I  F  E  T  K  F  Q  V  D  K  V  N  F  H

661        ATGTTTGACGTGGGTGGCCAGCGCGATGAACGCCGCAAGTGGATCCAGTGCTTCAACGAT
221         M  F  D  V  G  G  Q  R  D  E  R  R  K  W  I  Q  C  F  N  D

721        GTGACTGCCATCATCTTCGTGGTGGCCAGCAGCAGCTACAACATGGTCATCCGGGAGGAC
241         V  T  A  I  I  F  V  V  A  S  S  S  Y  N  M  V  I  R  E  D

781        AACCAGACCAACCGCCTGCAGGAGGCTCTGAACCTCTTCAAGAGCATCTGGAACAACAGA
261         N  Q  T  N  R  L  Q  E  A  L  N  L  F  K  S  I  W  N  N  R

841        TGGCTGCGCACCATCTCTGTGATCCTGTTCCTCAACAAGCAAGATCTGCTCGCTGAGAAA
281         W  L  R  T  I  S  V  I  L  F  L  N  K  Q  D  L  L  A  E  K

901        GTCCTTGCTGGGAAATCGAAGATTGAGGACTACTTTCCAGAATTTGCTCGCTACACTACT
301         V  L  A  G  K  S  K  I  E  D  Y  F  P  E  F  A  R  Y  T  T

961        CCTGAGGATGCTACTCCCGAGCCCGGAGAGGACCCACGCGTGACCCGGGCCAAGTACTTC
321         P  E  D  A  T  P  E  P  G  E  D  P  R  V  T  R  A  K  Y  F
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1021    ATTCGAGATGAGTTTCTGAGGATCAGCACTGCCAGTGGAGATGGGCGTCACTACTGCTAC
341      I  R  D  E  F  L  R  I  S  T  A  S  G  D  G  R  H  Y  C  Y

1081    CCTCATTTCACCTGCGCTGTGGACACTGAGAACATCCGCCGTGTGTTCAACGACTGCCGT
361      P  H  F  T  C  A  V  D  T  E  N  I  R  R  V  F  N  D  C  R

                                                          ClaI
1141    GACATCATTCAGCGCATGCACCTTCGTCAGTACGAGCTGCTCATCGAT
381      D  I  I  Q  R  M  H  L  R  Q  Y  E  L  L
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SEQ ID NO.: 194

Human Gαq

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        XhoI
1   CTCGAGATGACTCTGGAGTCCATCATGGCGTGCTGCCTGAGCGAGGAGGCCAAGGAAGCCCGGCGG
1        M  T  L  E  S  I  M  A  C  C  L  S  E  E  A  K  E  A  R  R

61      ATCAACGACGAGATCGAGCGGCAGCTCCGCAGGGACAAGCGGGACGCCCGCCGGGAGCTC
21       I  N  D  E  I  E  R  Q  L  R  R  D  K  R  D  A  R  R  E  L

121     AAGCTGCTGCTGCTCGGGACAGGAGAGAGTGGCAAGAGTACGTTTATCAAGCAGATGAGA
41       K  L  L  L  L  G  T  G  E  S  G  K  S  T  F  I  K  Q  M  R

181     ATCATCCATGGGTCAGGATACTCTGATGAAGATAAAAGGGGCTTCACCAAGCTGGTGTAT
61       I  I  H  G  S  G  Y  S  D  E  D  K  R  G  F  T  K  L  V  Y

241     CAGAACATCTTCACGGCCATGCAGGCCATGATCAGAGCCATGGACACACTCAAGATCCCA
81       Q  N  I  F  T  A  M  Q  A  M  I  R  A  M  D  T  L  K  I  P

301     TACAAGTATGAGCACAATAAGGCTCATGCACAATTAGTTCGAGAAGTTGATGTGGAGAAG
101      Y  K  Y  E  H  N  K  A  H  A  Q  L  V  R  E  V  D  V  E  K

361     GTGTCTGCTTTTGAGAATCCATATGTAGATGCAATAAAGAGTTTATGGAATGATCCTGGA
121      V  S  A  F  E  N  P  Y  V  D  A  I  K  S  L  W  N  D  P  G

421     ATCCAGGAATGCTATGATAGACGACGAGAATATCAATTATCTGACTCTACCAAATACTAT
141      I  Q  E  C  Y  D  R  R  R  E  Y  Q  L  S  D  S  T  K  Y  Y

481     CTTAATGACTTGGACCGCGTAGCTGACCCTGCCTACCTGCCTACGCAACAAGATGTGCTT
161      L  N  D  L  D  R  V  A  D  P  A  Y  L  P  T  Q  Q  D  V  L

541     AGAGTTCGAGTCCCCACCACAGGGATCATCGAATACCCCTTTGACTTACAAAGTGTCATT
181      R  V  R  V  P  T  T  G  I  I  E  Y  P  F  D  L  Q  S  V  I

601     TTCAGAATGGTCGATGTAGGGGGCCAAAGGTCAGAGAGAAGAAAATGGATACACTGCTTT
201      F  R  M  V  D  V  G  G  Q  R  S  E  R  R  K  W  I  H  C  F

661     GAAAATGTCACCTCTATCATGTTTCTAGTAGCGCTTAGTGAATATGATCAAGTTCTCGTG
221      E  N  V  T  S  I  M  F  L  V  A  L  S  E  Y  D  Q  V  L  V

721     GAGTCAGACAATGAGAACCGAATGGAGGAAAGCAAGGCTCTCTTTAGAACAATTATCACA
241      E  S  D  N  E  N  R  M  E  E  S  K  A  L  F  R  T  I  I  T

781     TACCCCTGGTTCCAGAACTCCTCGGTTATTCTGTTCTTAAACAAGAAAGATCTTCTAGAG
261      Y  P  W  F  Q  N  S  S  V  I  L  F  L  N  K  K  D  L  L  E
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841        GAGAAAATCATGTATTCCCATCTAGTCGACTACTTCCCAGAATATGATGGACCCCAGAGA
281         E  K  I  M  Y  S  H  L  V  D  Y  F  P  E  Y  D  G  P  Q  R

901        GATGCCCAGGCAGCCCGAGAATTCATTCTGAAGATGTTCGTGGACCTGAACCCAGACAGT
301         D  A  Q  A  A  R  E  F  I  L  K  M  F  V  D  L  N  P  D  S

961        GACAAAATTATCTACTCCCACTTCACGTGCGCCACAGACACCGAGAATATCCGCTTTGTC
321         D  K  I  I  Y  S  H  F  T  C  A  T  D  T  E  N  I  R  F  V

ClaI
1021
TTTGCTGCCGTCAAGGACACCATCCTCCAGTTGAACCTGAAGGAGTACAATCTGGTCATCGAT
341         F  A  A  V  K  D  T  I  L  Q  L  N  L  K  E  Y  N  L  V
```

SEQ ID NO.: 195

Human Giα

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     XhoI
1    CTCGAGATGGGCTGCACCGTGAGCGCCGAGGACAAGGCGGCGGCCGAGCGCTCTAAGATGATCGAC
1           M  G  C  T  V  S  A  E  D  K  A  A  A  E  R  S  K  M  I  D

61         AAGAACCTGCGGGAGGACGGAGAGAAGGCGGCGCGGGAGGTGAAGTTGCTGCTGTTGGGT
21          K  N  L  R  E  D  G  E  K  A  A  R  E  V  K  L  L  L  L  G

121        GCTGGGGAGTCAGGGAAGAGCACCATCGTCAAGCAGATGAAGATCATCCACGAGGATGGC
41          A  G  E  S  G  K  S  T  I  V  K  Q  M  K  I  I  H  E  D  G

181        TACTCCGAGGAGGAATGCCGGCAGTACCGGGCGGTTGTCTACAGCAACACCATCCAGTCC
61          Y  S  E  E  E  C  R  Q  Y  R  A  V  V  Y  S  N  T  I  Q  S

241        ATCATGGCCATTGTCAAAGCCATGGGAAACCTGCAGATCGACTTTGCCGACCCCTCCAGA
81          I  M  A  I  V  K  A  M  G  N  L  Q  I  D  F  A  D  P  S  R

301        GCGGACGACGCCAGGCAGCTATTTGCACTGTCCTGCACCGCCGAGGAGCAAGGCGTGCTC
101         A  D  D  A  R  Q  L  F  A  L  S  C  T  A  E  E  Q  G  V  L

361        CCTGATGACCTGTCCGGCGTCATCCGGAGGCTCTGGGCTGACCATGGTGTGCAGGCCTGC
121         P  D  D  L  S  G  V  I  R  R  L  W  A  D  H  G  V  Q  A  C

421        TTTGGCCGCTCAAGGGAATACCAGCTCAACGACTCAGCTGCCTACTACCTGAACGACCTG
141         F  G  R  S  R  E  Y  Q  L  N  D  S  A  A  Y  Y  L  N  D  L

481        GAGCGTATTGCACAGAGTGACTACATCCCCACACAGCAAGATGTGCTACGGACCCGCGTA
161         E  R  I  A  Q  S  D  Y  I  P  T  Q  Q  D  V  L  R  T  R  V

541        AAGACCACGGGGATCGTGGAGACACACTTCACCTTCAAGGACCTACACTTCAAGATGTTT
181         K  T  T  G  I  V  E  T  H  F  T  F  K  D  L  H  F  K  M  F

601        GATGTGGGTGGTCAGCGGTCTGAGCGGAAGAAGTGGATCCACTGCTTTGAGGGCGTCACA
201         D  V  G  G  Q  R  S  E  R  K  K  W  I  H  C  F  E  G  V  T

661        GCCATCATCTTCTGCGTAGCCTTGAGCGCCTATGACTTGGTGCTAGCTGAGGACGAGGAG
221         A  I  I  F  C  V  A  L  S  A  Y  D  L  V  L  A  E  D  E  E
```

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721     ATGAACCGCATGCATGAGAGCATGAAGCTATTCGATAGCATCTGCAACAACAAGTGGTTC
241      M  N  R  M  H  E  S  M  K  L  F  D  S  I  C  N  N  K  W  F

781     ACAGACACGTCCATCATCCTCTTCCTCAACAAGAAGGACCTGTTTGAGGAGAAGATCACA
261      T  D  T  S  I  I  L  F  L  N  K  K  D  L  F  E  E  K  I  T

841     CACAGTCCCCTGACCATCTGCTTCCCTGAGTACACAGGGGCCAACAAATATGATGAGGCA
281      H  S  P  L  T  I  C  F  P  E  Y  T  G  A  N  K  Y  D  E  A

901     GCCAGCTACATCCAGAGTAAGTTTGAGGACCTGAATAAGCGCAAAGACACCAAGGAGATC
301      A  S  Y  I  Q  S  K  F  E  D  L  N  K  R  K  D  T  K  E  I

961     TACACGCACTTCACGTGCGCCACCGACACCAAGAACGTGCAGTTCGTGTTTGACGCCGTC
321      Y  T  H  F  T  C  A  T  D  T  K  N  V  Q  F  V  F  D  A  V

                                                          ClaI
1021    ACCGATGTCATCATCAAGAACAACCTGAAGGACTGCGGCCTCTTCATGCAT
341      T  D  V  I  I  K  N  N  L  K  D  C  G  L  F
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SEQ ID NO.: 196

Human Gα12/13

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        XhoI
1   CTCGAGATGTCCGGGGTGGTGCGGACCCTCAGCCGCTGCCTGCTGCCGGCCGAGGCCGGCGGGGCC
1        M  S  G  V  V  R  T  L  S  R  C  L  L  P  A  E  A  G  G  A

61      CGCGAGCGCAGGGCGGGCAGCGGCGCGCGCGACGCGGAGCGCGAGGCCCGGAGGCGTAGC
21       R  E  R  R  A  G  S  G  A  R  D  A  E  R  E  A  R  R  S

121     CGCGACATCGACGCGCTGCTGGCCCGCGAGCGGCGCGCGGTCCGGCGCCTGGTGAAGATC
41       R  D  I  D  A  L  L  A  R  E  R  R  A  V  R  R  L  V  K  I

181     CTGCTGCTGGGCGCGGGCGAGAGCGGCAAGTCCACGTTCCTCAAGCAGATGCGCATCATC
61       L  L  L  G  A  G  E  S  G  K  S  T  F  L  K  Q  M  R  I  I

241     CACGGCCGCGAGTTCGACCAGAAGGCGCTGCTGGAGTTCCGCGACACCATCTTCGACAAC
81       H  G  R  E  F  D  Q  K  A  L  L  E  F  R  D  T  I  F  D  N

301     ATCCTCAAGGGCTCAAGGGTTCTTGTTGATGCACGAGATAAGCTTGGCATTCCTTGGCAG
101      I  L  K  G  S  R  V  L  V  D  A  R  D  K  L  G  I  P  W  Q

361     TATTCTGAAAATGAGAAGCATGGGATGTTCCTGATGGCCTTCGAGAACAAGGCGGGGCTG
121      Y  S  E  N  E  K  H  G  M  F  L  M  A  F  E  N  K  A  G  L

421     CCTGTGGAGCCGGCCACCTTCCAGCTGTACGTCCCGGCCCTGAGCGCACTCTGGAGGGAT
141      P  V  E  P  A  T  F  Q  L  Y  V  P  A  L  S  A  L  W  R  D

481     TCTGGCATCAGGGAGGCTTTCAGCCGGAGAAGCGAGTTTCAGCTGGGGGAGTCGGTGAAG
161      S  G  I  R  E  A  F  S  R  R  S  E  F  Q  L  G  E  S  V  K

541     TACTTCCTGGACAACTTGGACCGGATCGGCCAGCTGAATTACTTTCCTAGTAAGCAAGAT
181      Y  F  L  D  N  L  D  R  I  G  Q  L  N  Y  F  P  S  K  Q  D

601     ATCCTGCTGGCTAGGAAAGCCACCAAGGGAATTGTGGAGCATGACTTCGTTATTAAGAAG
201      I  L  L  A  R  K  A  T  K  G  I  V  E  H  D  F  V  I  K  K
```

```
661     ATCCCCTTTAAGATGGTGGATGTGGGCGGCCAGCGGTCCCAGCGCCAGAAGTGGTTCCAG
221      I  P  F  K  M  V  D  V  G  G  Q  R  S  Q  R  Q  K  W  F  Q

721     TGCTTCGACGGGATCACGTCCATCCTGTTCATGGTCTCCTCCAGCGAGTACGACCAGGTC
241      C  F  D  G  I  T  S  I  L  F  M  V  S  S  S  E  Y  D  Q  V

781     CTCATGGAGGACAGGCGCACCAACCGGCTGGTGGAGTCCATGAACATCTTCGAGACCATC
261      L  M  E  D  R  R  T  N  R  L  V  E  S  M  N  I  F  E  T  I

841     GTCAACAACAAGCTCTTCTTCAACGTCTCCATCATTCTCTTCCTCAACAAGATGGACCTC
281      V  N  N  K  L  F  F  N  V  S  I  I  L  F  L  N  K  M  D  L

901     CTGGTGGAGAAGGTGAAGACCGTGAGCATCAAGAAGCACTTCCCGGACTTCAGGGGCGAC
301      L  V  E  K  V  K  T  V  S  I  K  K  H  F  P  D  F  R  G  D

961     CCGCACCAGCTGGAGGACGTCCAGCGCTACCTGGTCCAGTGCTTCGACAGGAAGAGACGG
321      P  H  Q  L  E  D  V  Q  R  Y  L  V  Q  C  F  D  R  K  R  R

1021    AACCGCAGCAAGCCACTCTTCCACCACTTCACCACCGCCATCGACACCGAGAACGTCCGC
341      N  R  S  K  P  L  F  H  H  F  T  T  A  I  D  T  E  N  V  R

1081    TTCGTGTTCCATGCTGTGAAAGACACCATCCTGCAGGAGAACCTGAAGGACATCATGCTG
361      F  V  F  H  A  V  K  D  T  I  L  Q  E  N  L  K  D  I  M  L

            ClaI
1141    CAGATCGAT
381      Q
```

SEQ ID NO.: 205

Human β2AR-ToxR (5-141) chimera stop GS1α-ToxR (5-141) chimera transcriptional fusion

```
        SalI  +1 B2AR
1       GTCGACATGG GGCAACCCGG GAACGGCAGC GCCTTCTTGC TGGCACCCAA
TGGAAGCCAT

61      GCGCCGGACC ACGACGTCAC GCAGCAAAGG GACGAGGTGT GGGTGGTGGG
CATGGGCATC
121     GTCATGTCTC TCATCGTCCT GGCCATCGTG TTTGGCAATG TGCTGGTCAT
CACAGCCATT
181     GCCAAGTTCG AGCGTCTGCA GACGGTCACC AACTACTTCA TCACTTCACT
GGCCTGTGCT
241     GATCTGGTCA TGGGCCTAGC AGTGGTGCCC TTTGGGGCCG CCCATATTCT
TATGAAAATG
301     TGGACTTTTG GCAACTTCTG GTGCGAGTTT TGGACTTCCA TTGATGTGCT
GTGCGTCACG
361     GCCAGCATTG AGACCCTGTG CGTGATCGCA GTGGATCGCT ACTTTGCCAT
TACTTCACCT
```

421 TTCAAGTACC AGAGCCTGCT GACCAAGAAT AAGGCCCGGG TGATCATTCT
GATGGTGTGG
481 ATTGTGTCAG GCCTTAYCTC CTTCTTGCCC ATTCAGATGC ACTGGTACAG
GGCCACCCAC
541 CAGGAAGCCA TCAACTGCTA TGCCAATGAG ACCTGCTGTG ACTTCTTCAC
GAACCAAGCC
601 TATGCCATTG CCTCTTCCAT CGTGTCCTTC TACGTTCCCC TGGTGATCAT
GGTCTTCGTC
661 TACTCCAGGG TCTTTCAGGA GGCCAAAAGG CAGCTCCAGA AGATTGACAA
ATCTGAGGGC
721 CGCTTCCATG TCCAGAACCT TAGCCAGGTG GAGCAGGATG GGCGGACGGG
GCATGGACTC
781 CGCAGATCTT CCAAGTTCTG CTTGAAGGAG CACAAAGCCC TCAAGACGTT
AGGCATCATC
841 ATGGGCACTT TCACCCTCTG CTGGCTGCCC TTCTTCATCG TTAACATTGT
GCATGTGATC
901 CAGGATAACC TCATCCGTAA GGAAGTTTAC ATCCTCCTAA ATTGGATAGG
CTATGTCAAT
961 TCTGGTTTCA ATCCCCTTAT CTACTGCCGG AGCCCAGATT TCAGGATTGC
CTTCCAGGAG
1021 CTTCTGTGCC TGCGCAGGTC TTCTTTGAAG GCCTATGGCA ATGGCTACTC
CAGCAACGGC
1081 AACACAGGGG AGCAGAGTGG ATATCACGTG GAACAGGAGA AAGAAAATAA
ACTGCTGTGT
1141 GAAGACCTCC CAGGCACGGA AGACTTTGTG GGCCATCAAG GTACTGTGCC
TAGCGATAAC

last B2AR linker

sequence
1201 ATTGATTCAC AAGGGAGGAA TTGTAGTACA AATGACTCAC TGCTA**GAGCG**
TGGCCAGACG

PstI +5 toxR (5-141)
1261 **GTCACCAACC** TGCAG**GGA**CA CAACTCAAAA GAGATATCGA TGAGTCATAT
TGGTACTAAA

1321 TTCATTCTTG CTGAAAAATT TACCTTCGAT CCCCTAAGCA ATACTCTGAT
TGACAAAGAA
1381 GATAGTGAAG AGATCATTCG ATTAGGCAGC AACGAAAGCC GAATTCTTTG
GCTGCTGGCC
1441 CAACGTCCAA ACGAGGTAAT TTCTCGCAAT GATTTGCATG ACTTTGTTTG
GCGAGAGCAA
1501 GGTTTTGAAG TCGATGATTC CAGCTTAACC CAAGCCATTT CGACTCTGCG
CAAAATGCTC
1561 AAAGATTCGA CAAAGTCCCC ACAATACGTC AAAACGGTTC CGAAGCGCGG
TTACCAATTG
1621 ATCGCCCGAG TGGAAACGGT TGAAGAAGAG ATGGCTCGCG AAAACGAAGC
TGCTCATGAC

stop SD XhoI +1 GS1 alpha
1681 ATCTCT**TAAT** **AA**TCAAGGAG GCCCTCGAGA TGGGCTGCCT CGGGAACAGT
AAGACCGAGG

1741 ACCAGCGCAA CGAGGAGAAG GCGCAGCGTG AGGCCAACAA AAAGATCGAG
AAGCAGCTGC
1801 AGAAGGACAA GCAGGTCTAC CGGGCCACGC ACCGCCTGCT GCTGCTGGGT
GCTGGAGAAT

1861 CTGGTAAAAG CACCATTGTG AAGCAGATGA GGATCCTGCA TGTTAATGGG
TTTAATGGAG
1921 ACAGTGAGAA GGCAACCAAA GTGCAGGACA TCAAAAACAA CCTGAAAGAG
GCGATTGAAA
1981 CCATTGTGGC CGCCATGAGC AACCTGGTGC CCCCCGTGGA GCTGGCCAAC
CCCGAGAACC
2041 AGTTCAGAGT GGACTACATC CTGAGTGTGA TGAACGTGCC TGACTTTGAC
TTCCCTCCCG
2101 AATTCTATGA GCATGCCAAG GCTCTGTGGG AGGATGAAGG AGTGCGTGCC
TGCTACGAAC
2161 GCTCCAACGA GTACCAGCTG ATTGACTGTG CCCAGTACTT CCTGGACAAG
ATCGACGTGA
2221 TCAAGCAGGC TGACTATGTG CCGAGCGATC AGGACCTGCT TCGCTGCCGT
GTCCTGACTT
2281 CTGGAATCTT TGAGACCAAG TTCCAGGTGG ACAAAGTCAA CTTCCACATG
TTTGACGTGG
2341 GTGGCCAGCG CGATGAACGC CGCAAGTGGA TCCAGTGCTT CAACGATGTG
ACTGCCATCA
2401 TCTTCGTGGT GGCCAGCAGC AGCTACAACA TGGTCATCCG GGAGGACAAC
CAGACCAACC
2461 GCCTGCAGGA GGCTCTGAAC CTCTTCAAGA GCATCTGGAA CAACAGATGG
CTGCGCACCA
2521 TCTCTGTGAT CCTGTTCCTC AACAAGCAAG ATCTGCTCGC TGAGAAAGTC
CTTGCTGGGA
2581 AATCGAAGAT TGAGGACTAC TTTCCAGAAT TTGCTCGCTA CACTACTCCT
GAGGATGCTA
2641 CTCCCGAGCC CGGAGAGGAC CCACGCGTGA CCCGGGCCAA GTACTTCATT
CGAGATGAGT
2701 TTCTGAGGAT CAGCACTGCC AGTGGAGATG GGCGTCACTA CTGCTACCCT
CATTTCACCT
2761 GCGCTGTGGA CACTGAGAAC ATCCGCCGTG TGTTCAACGA CTGCCGTGAC
ATCATTCAGC

ClaI +5 toxR (5-141)
2821 GCATGCACCT TCGTCAGTAC GAGCTGCTCA TCGATGGACA CAACTCAAAA
GAGATATCGA

2881 TGAGTCATAT TGGTACTAAA TTCATTCTTG CTGAAAAATT TACCTTCGAT
CCCCTAAGCA
2941 ATACTCTGAT TGACAAAGAA GATAGTGAAG AGATCATTCG ATTAGGCAGC
AACGAAAGCC
3001 GAATTCTTTG GCTGCTGGCC CAACGTCCAA ACGAGGTAAT TTCTCGCAAT
GATTTGCATG
3061 ACTTTGTTTG GCGAGAGCAA GGTTTTGAAG TCGATGATTC CAGCTTAACC
CAAGCCATTT
3121 CGACTCTGCG CAAAATGCTC AAAGATTCGA CAAAGTCCCC ACAATACGTC
AAAACGGTTC
3181 CGAAGCGCGG TTACCAATTG ATCGCCCGAG TGGAAACGGT TGAAGAAGAG
ATGGCTCGCG

Stop XbaI Stem-loop
3241 AAAACGAAGC TGCTCATGAC ATCTCTTAAT AATCTAGAGG ATCCCCGCGC
CCTCATCCGA

3301 AAGGGCG

SEQ ID NO.: 208

Vibrio cholerae Pctx::lacZ reporter fusion constuct

XbaI
1 TCTAGAGGCT GTGGGTAGAA GTGAAACGGG GTTTACCGAT AAAAACAGAA
AATGATAAAA

3 ToxR binding repeats
61 AAGGACTAAA TAGTATATTT TGATTTTTGA TTTTTGATTT CAAATAATAC
AAATTTATTT

+1

lacZ
121 ACTTATTTAA TTGTTTTGAT CAATTATTTT TCTGTTAAAC AAAGGGAGCA
TTATATGGTA

181 AAGACCATGA TTACGGATTC ACTGGCCGTC GTTTTACAAC GTCGTGACTG
GGAAAACCCT
241 GGCGTTACCC AACTTAATCG CCTTGCAGCA CATCCCCCTT TCGCCAGCTG
GCGTAATAGC
301 GAAGAGGCCC GCACCGATCG CCCTTCCCAA CAGTTGCGCA GCCTGAATGG
CGAATGGCGC
361 TTTGCCTGGT TTCCGGCACC AGAAGCGGTG CCGGAAAGCT GGCTGGAGTG
CGATCTTCCT
421 GAGGCCGATA CTGTCGTCGT CCCCTCAAAC TGGCAGATGC ACGGTTACGA
TGCGCCCATC
481 TACACCAACG TGACCTATCC CATTACGGTC AATCCGCCGT TTGTTCCCAC
GGAGAATCCG
541 ACGGGTTGTT ACTCGCTCAC ATTTAATGTT GATGAAAGCT GGCTACAGGA
AGGCCAGACG
601 CGAATTATTT TTGATGGCGT TAACTCGGCG TTTCATCTGT GGTGCAACGG
GCGCTGGGTC
661 GGTTACGGCC AGGACAGTCG TTTGCCGTCT GAATTTGACC TGAGCGCATT
TTTACGCGCC
721 GGAGAAAACC GCCTCGCGGT GATGGTGCTG CGCTGGAGTG ACGGCAGTTA
TCTGGAAGAT,
781 CAGGATATGT GGCGGATGAG CGGCATTTTC CGTGACGTCT CGTTGCTGCA
TAAACCGACT
841 ACACAAATCA GCGATTTCCA TGTTGCCACT CGCTTTAATG ATGATTTCAG
CCGCGCTGTA
901 CTGGAGGCTG AAGTTCAGAT GTGCGGCGAG TTGCGTGACT ACCTACGGGT
AACAGTTTCT
961 TTATGGCAGG GTGAAACGCA GGTCGCCAGC GGCACCGCGC CTTTCGGCGG
TGAAATTATC
1021 GATGAGCGTG GTGGTTATGC CGATCGCGTC ACACTACGTC TGAACGTCGA
AAACCCGAAA
1081 CTGTGGAGCG CCGAAATCCC GAATCTCTAT CGTGCGGTGG TTGAACTGCA
CACCGCCGAC
1141 GGCACGCTGA TTGAAGCAGA AGCCTGCGAT GTCGGTTTCC GCGAGGTGCG
GATTGAAAAT
1201 GGTCTGCTGC TGCTGAACGG CAAGCCGTTG CTGATTCGAG GCGTTAACCG
TCACGAGCAT
1261 CATCCTCTGC ATGGTCAGGT CATGGATGAG CAGACGATGG TGCAGGATAT
CCTGCTGATG
1321 AAGCAGAACA ACTTTAACGC CGTGCGCTGT TCGCATTATC CGAACCATCC
GCTGTGGTAC

1381 ACGCTGTGCG ACCGCTACGG CCTGTATGTG GTGGATGAAG CCAATATTGA AACCCACGGC
1441 ATGGTGCCAA TGAATCGTCT GACCGATGAT CCGCGCTGGC TACCGGCGAT GAGCGAACGC
1501 GTAACGCGAA TGGTGCAGCG CGATCGTAAT CACCCGAGTG TGATCATCTG GTCGCTGGGG
1561 AATGAATCAG GCCACGGCGC TAATCACGAC GCGCTGTATC GCTGGATCAA ATCTGTCGAT
1621 CCTTCCCGCC CGGTGCAGTA TGAAGGCGGC GGAGCCGACA CCACGGCCAC CGATATTATT
1681 TGCCCGATGT ACGCGCGCGT GGATGAAGAC CAGCCCTTCC CGGCTGTGCC GAAATGGTCC
1741 ATCAAAAAAT GGCTTTCGCT ACCTGGAGAG ACGCGCCCGC TGATCCTTTG CGAATACGCC
1801 CACGCGATGG GTAACAGTCT TGGCGGTTTC GCTAAATACT GGCAGGCGTT TCGTCAGTAT
1861 CCCCGTTTAC AGGGCGGCTT CGTCTGGGAC TGGGTGGATC AGTCGCTGAT TAAATATGAT
1921 GAAAACGGCA ACCCGTGGTC GGCTTACGGC GGTGATTTTG GCGATACGCC GAACGATCGC
1981 CAGTTCTGTA TGAACGGTCT GGTCTTTGCC GACCGCACGC CGCATCCAGC GCTGACGGAA
2041 GCAAAACACC AGCAGCAGTT TTTCCAGTTC CGTTTATCCG GGCAAACCAT CGAAGTGACC
2101 AGCGAATACC TGTTCCGTCA TAGCGATAAC GAGCTCCTGC ACTGGATGGT GGCGCTGGAT
2161 GGTAAGCCGC TGGCAAGCGG TGAAGTGCCT CTGGATGTCG CTCCACAAGG TAAACAGTTG
2221 ATTGAACTGC CTGAACTACC GCAGCCGGAG AGCGCCGGGC AACTCTGGCT CACAGTACGC
2281 GTAGTGCAAC CGAACGCGAC CGCATGGTCA GAAGCCGGGC ACATCAGCGC CTGGCAGCAG
2341 TGGCGTCTGG CGGAAAACCT CAGTGTGACG CTCCCCGCCG CGTCCCACGC CATCCCGCAT
2401 CTGACCACCA GCGAAATGGA TTTTTGCATC GAGCTGGGTA ATAAGCGTTG GCAATTTAAC
2461 CGCCAGTCAG GCTTTCTTTC ACAGATGTGG ATTGGCGATA AAAAACAACT GCTGACGCCG
2521 CTGCGCGATC AGTTCACCCG TGCACCGCTG GATAACGACA TTGGCGTAAG TGAAGCGACC
2581 CGCATTGACC CTAACGCCTG GGTCGAACGC TGGAAGGCGG CGGGCCATTA CCAGGCCGAA
2641 GCAGCGTTGT TGCAGTGCAC GGCAGATACA CTTGCTGATG CGGTGCTGAT TACGACCGCT
2701 CACGCGTGGC AGCATCAGGG GAAAACCTTA TTTATCAGCC GGAAAACCTA CCGGATTGAT
2761 GGTAGTGGTC AAATGGCGAT TACCGTTGAT GTTGAAGTGG CGAGCGATAC ACCGCATCCG
2821 GCGCGGATTG GCCTGAACTG CCAGCTGGCG CAGGTAGCAG AGCGGGTAAA CTGGCTCGGA
2881 TTAGGGCCGC AAGAAAACTA TCCCGACCGC CTTACTGCCG CCTGTTTTGA CCGCTGGGAT
2941 CTGCCATTGT CAGACATGTA TACCCCGTAC GTCTTCCCGA GCGAAAACGG TCTGCGCTGC
3001 GGGACGCGCG AATTGAATTA TGGCCCACAC CAGTGGCGCG GCGACTTCCA GTTCAACATC
3061 AGCCGCTACA GTCAACAGCA ACTGATGGAA ACCAGCCATC GCCATCTGCT GCACGCGGAA
3121 GAAGGCACAT GGCTGAATAT CGACGGTTTC CATATGGGGA TTGGTGGCGA CGACTCCTGG

3181 AGCCCGTCAG TATCGGCGGA ATTCCAGCTG AGCGCCGGTC GCTACCATTA
CCAGTTGGTC

Stop Stem-loop XbaI
3241 TGGTGTCAAA AATAATAACGCCCTCAT CCGAAAGGGC GTCTAGA

SEQ ID NO.: 266

pMPX-74 MalE (1-28) fusion vector

SD old PstI +1
2401 GAATTCAGGCGCTTTTTAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCATATGAAAAT
1 M K I

2461 AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTC
4 K T G A R I L A L S A L T T M M F S A S

Factor Xa PstI SalI XbaI
2521 GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCTAGAGA
24 A L A K I I E A R L Q A S V D A E S R D

FLAG lost XbaI
2581 TTATAAAGATGACGATGACAAATAATAAGCTAGAGG (transcriptional stop)
44 Y K D D D D K

pMPX-72::malE(1-28)::FXa::PstI, SalI, XbaI::FLAG
Rhamnose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-72 cut with PstI & XbaI.

SEQ ID NO.: 267

pMPX-75 MalE (1-28) fusion vector

SD old PstI +1
1621 CCATACCCGTTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAAACAGGTGCAC
1 M K I K T G A

1681 GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCCAAAA
8 R I L A L S A L T T M M F S A S A L A K

Factor Xa PstI SalI XbaI FLAG
1741 TCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCTAGAGATTATAAAGATGACG

Lost XbaI
1801 ATGACAAATAATAAGCTAGAGG (Transcriptional stop)

pMPX-71::malE(1-28)::FXa::PstI, SalI, XbaI::FLAG
Arabinose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-71 cut with PstI & XbaI.

SEQ ID NO.: 268

pMPX-88 MalE (1-28) fusion vector

```
                                                    SD  old PstI  +1
                                                   AGGAGGTTCTGCATATGAAAAT
1                                                                M  K  I

          AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTC
4           K  T  G  A  R  I  L  A  L  S  A  L  T  T  M  M  F  S  A  S

                              Factor Xa   PstI        SalI        XbaI
          GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCTAGAGA
24          A  L  A  K  I  I  E  A  R  L  Q  A  S  V  D  A  E  S  R  D

                    FLAG                lost XbaI
          TTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC (transcriptional
stop)
44          Y  K  D  D  D  D  K
```

pMPX-84::malE(1-28)::FXa::PstI, SalI, XbaI::FLAG
Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-84 cut with PstI & XbaI.

SEQ ID NO.: 269

pMPX-93 MalE (1-28) fusion vector

```
                                                    SD  old PstI  +1
                                                   AGGAGGTTCTGCATATGAAAAT
1                                                                M  K  I

          AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTC
4           K  T  G  A  R  I  L  A  L  S  A  L  T  T  M  M  F  S  A  S

                              Factor Xa   PstI        SalI        XbaI
          GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCTAGAGA
24          A  L  A  K  I  I  E  A  R  L  Q  A  S  V  D  A  E  S  R  D

                    FLAG                lost XbaI
          TTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC (transcriptional
stop)
44          Y  K  D  D  D  D  K
```

pMPX-86::malE(1-28)::FXa::PstI, SalI, XbaI::FLAG
Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-86 cut with PstI & XbaI.

SEQ ID NO.: 270

pMPX-77 MalE (1-370 del 354-364) fusion vector

```
                                                                SD  old PstI  +1
2401    GAATTCAGGCGCTTTTTAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCATATGAAAAT
1                                                                   M  K  I

2461    AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTC
4         K  T  G  A  R  I  L  A  L  S  A  L  T  T  M  M  F  S  A  S

2521    GGCTCTCGCCAAAATCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTA
24        A  L  A  K  I  E  E  G  K  L  V  I  W  I  N  G  D  K  G  Y

2581    TAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGT
44        N  G  L  A  E  V  G  K  K  F  E  K  D  T  G  I  K  V  T  V

2641    TGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCC
64        E  H  P  D  K  L  E  E  K  F  P  Q  V  A  A  T  G  D  G  P

2701    TGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGC
84        D  I  I  F  W  A  H  D  R  F  G  G  Y  A  Q  S  G  L  L  A

2761    TGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGT
104       E  I  T  P  D  K  A  F  Q  D  K  L  Y  P  F  T  W  D  A  V

2821    ACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTA
124       R  Y  N  G  K  L  I  A  Y  P  I  A  V  E  A  L  S  L  I  Y

2881    TAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAA
144       N  K  D  L  L  P  N  P  P  K  T  W  E  E  I  P  A  L  D  K

2941    AGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCAC
164       E  L  K  A  K  G  K  S  A  L  M  F  N  L  Q  E  P  Y  F  T

3001    CTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGA
184       W  P  L  I  A  A  D  G  G  Y  A  F  K  Y  E  N  G  K  Y  D

3061    CATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGA
204       I  K  D  V  G  V  D  N  A  G  A  K  A  G  L  T  F  L  V  D

3121    CCTGATTAAAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTT
224       L  I  K  N  K  H  M  N  A  D  T  D  Y  S  I  A  E  A  A  F

3181    TAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACAC
244       N  K  G  E  T  A  M  T  I  N  G  P  W  A  W  S  N  I  D  T

3241    CAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACC
264       S  K  V  N  Y  G  V  T  V  L  P  T  F  K  G  Q  P  S  K  P

3301    GTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAA
```

```
284          F  V  G  V  L  S  A  G  I  N  A  A  S  P  N  K  E  L  A  K

3361      AGAGTTCCTCGAAAACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAA
304         E  F  L  E  N  Y  L  L  T  D  E  G  L  E  A  V  N  K  D  K

3421      ACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTAT
324         P  L  G  A  V  A  L  K  S  Y  E  E  E  L  A  K  D  P  R  I
```

pMPX-72::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG
Rhamnose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-72 cut with PstI & XbaI.

SEQ ID NO.: 271

pMPX-76 MalE (1-370 del 354-364) fusion vector

```
                                                SD  old PstI +1
1621      CCATACCCGTTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAAACAGGTGCAC
1                                                       M  K  I  K  T  G  A

1681      GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCCAAAA
8         R  I  L  A  L  S  A  L  T  T  M  M  F  S  A  S  A  L  A  K

1741      TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCTCGCTG
28        I  E  E  G  K  L  V  I  W  I  N  G  D  K  G  Y  N  G  L  A

1801      AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCCGGATA
48        E  V  G  K  K  F  E  K  D  T  G  I  K  V  T  V  E  H  P  D

1861      AACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCT
68        K  L  E  E  K  F  P  Q  V  A  A  T  G  D  G  P  D  I  I  F

1921      GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGG
88        W  A  H  D  R  F  G  G  Y  A  Q  S  G  L  L  A  E  I  T  P

1981      ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAACGGCA
108       D  K  A  F  Q  D  K  L  Y  P  F  T  W  D  A  V  R  Y  N  G

2041      AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGATCTGC
128       K  L  I  A  Y  P  I  A  V  E  A  L  S  L  I  Y  N  K  D  L

2101      TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGAAAGCGA
148       L  P  N  P  P  K  T  W  E  E  I  P  A  L  D  K  E  L  K  A

2161      AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCTGATTG
168       K  G  K  S  A  L  M  F  N  L  Q  E  P  Y  F  T  W  P  L  I

2221      CTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGACGTGG
188       A  A  D  G  G  Y  A  F  K  Y  E  N  G  K  Y  D  I  K  D  V

2281      GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAAAAACA
208       G  V  D  N  A  G  A  K  A  G  L  T  F  L  V  D  L  I  K  N

2341      AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAA
228       K  H  M  N  A  D  T  D  Y  S  I  A  E  A  A  F  N  K  G  E
```

```
2401      CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTGAATT
248       T  A  M  T  I  N  G  P  W  A  W  S  N  I  D  T  S  K  V  N

2461      ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGGCGTGC
268       Y  G  V  T  V  L  P  T  F  K  G  Q  P  S  K  P  F  V  G  V

2521      TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCTCGAAA
288       L  S  A  G  I  N  A  A  S  P  N  K  E  L  A  K  E  F  L  E

2581      ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGGTGCCG
308       N  Y  L  L  T  D  E  G  L  E  A  V  N  K  D  K  P  L  G  A

2641      TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCACCATGG
328       V  A  L  K  S  Y  E  E  E  L  A  K  D  P  R  I  A  A  T  M

                                                  Factor Xa   PstI
2701      AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGCCTCGG
348       E  N  A  Q  S  A  F  W  Y  A  V  R  I  E  A  R  L  Q  A  S

          SalI        XbaI            FLAG              Lost XbaI
2761
TCGACGCCGAATCTAGAGATTATAAAGATGACGATGACAAATAATAAGCTAGAGGA(trxn stop)
368       V  D  A  E  S  R  D  Y  K  D  D  D  D  K
```

pMPX-71::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG
Arabinose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-71 cut with PstI & XbaI.

SEQ ID NO.: 272

pMPX-89 MalE (1-370 del 354-364) fusion vector

```
                                    SD  old PstI +1
                                    AGGAGGTTCTGCATATGAAAATAAAAACAGGTGCAC
1                                                   M  K  I  K  T  G  A

          GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCCAAAA
8         R  I  L  A  L  S  A  L  T  T  M  M  F  S  A  S  A  L  A  K

          TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCTCGCTG
28        I  E  E  G  K  L  V  I  W  I  N  G  D  K  G  Y  N  G  L  A

          AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCCGGATA
48        E  V  G  K  K  F  E  K  D  T  G  I  K  V  T  V  E  H  P  D

          AACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCT
68        K  L  E  E  K  F  P  Q  V  A  A  T  G  D  G  P  D  I  I  F

          GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGG
88        W  A  H  D  R  F  G  G  Y  A  Q  S  G  L  L  A  E  I  T  P
```

```
            ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAACGGCA
108         D  K  A  F  Q  D  K  L  Y  P  F  T  W  D  A  V  R  Y  N  G

            AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGATCTGC
128         K  L  I  A  Y  P  I  A  V  E  A  L  S  L  I  Y  N  K  D  L

            TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGAAAGCGA
148         L  P  N  P  P  K  T  W  E  E  I  P  A  L  D  K  E  L  K  A

            AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCTGATTG
168         K  G  K  S  A  L  M  F  N  L  Q  E  P  Y  F  T  W  P  L  I

            CTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGACGTGG
188         A  A  D  G  G  Y  A  F  K  Y  E  N  G  K  Y  D  I  K  D  V

            GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAAAAACA
208         G  V  D  N  A  G  A  K  A  G  L  T  F  L  V  D  L  I  K  N

            AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAA
228         K  H  M  N  A  D  T  D  Y  S  I  A  E  A  A  F  N  K  G  E

            CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTGAATT
248         T  A  M  T  I  N  G  P  W  A  W  S  N  I  D  T  S  K  V  N

            ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGGCGTGC
268         Y  G  V  T  V  L  P  T  F  K  G  Q  P  S  K  P  F  V  G  V

            TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCTCGAAA
288         L  S  A  G  I  N  A  A  S  P  N  K  E  L  A  K  E  F  L  E

            ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGGTGCCG
308         N  Y  L  L  T  D  E  G  L  E  A  V  N  K  D  K  P  L  G  A

            TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCACCATGG
328         V  A  L  K  S  Y  E  E  E  L  A  K  D  P  R  I  A  A  T  M

                                                    Factor Xa   PstI
            AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGCCTCGG
348         E  N  A  Q  S  A  F  W  Y  A  V  R  I  E  A  R  L  Q  A  S

            SalI        XbaI            FLAG              Lost XbaI
            TCGACGCCGAATCTAGAGATTATAAAGATGACGATGACAAATAATAAGCTAGAGG
(trxn stop)
368         V  D  A  E  S  R  D  Y  K  D  D  D  D  K
```

pMPX-84::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG
Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-84 cut with PstI & XbaI.

SEQ ID NO.: 273

pMPX-94 MalE (1-370 del 354-364) fusion vector

```
                                  SD  old PstI +1
AGGAGGTTCTGCATATGAAAATAAAAACAGGTGCAC
```

```
1                                                        M  K  I  K  T  G  A

   GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCCAAAA
8  R  I  L  A  L  S  A  L  T  T  M  M  F  S  A  S  A  L  A  K

   TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCTCGCTG
28 I  E  E  G  K  L  V  I  W  I  N  G  D  K  G  Y  N  G  L  A

   AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCCGGATA
48 E  V  G  K  K  F  E  K  D  T  G  I  K  V  T  V  E  H  P  D

   AACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCT
68 K  L  E  E  K  F  P  Q  V  A  A  T  G  D  G  P  D  I  I  F

   GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGG
88 W  A  H  D  R  F  G  G  Y  A  Q  S  G  L  L  A  E  I  T  P

   ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAACGGCA
108 D  K  A  F  Q  D  K  L  Y  P  F  T  W  D  A  V  R  Y  N  G

   AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGATCTGC
128 K  L  I  A  Y  P  I  A  V  E  A  L  S  L  I  Y  N  K  D  L

   TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGAAAGCGA
148 L  P  N  P  P  K  T  W  E  E  I  P  A  L  D  K  E  L  K  A

   AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCTGATTG
168 K  G  K  S  A  L  M  F  N  L  Q  E  P  Y  F  T  W  P  L  I

   CTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGACGTGG
188 A  A  D  G  G  Y  A  F  K  Y  E  N  G  K  Y  D  I  K  D  V

   GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAAAAACA
208 G  V  D  N  A  G  A  K  A  G  L  T  F  L  V  D  L  I  K  N

   AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAA
228 K  H  M  N  A  D  T  D  Y  S  I  A  E  A  A  F  N  K  G  E

   CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTGAATT
248 T  A  M  T  I  N  G  P  W  A  W  S  N  I  D  T  S  K  V  N

   ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGGCGTGC
268 Y  G  V  T  V  L  P  T  F  K  G  Q  P  S  K  P  F  V  G  V

   TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCTCGAAA
288 L  S  A  G  I  N  A  A  S  P  N  K  E  L  A  K  E  F  L  E

   ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGGTGCCG
308 N  Y  L  L  T  D  E  G  L  E  A  V  N  K  D  K  P  L  G  A

   TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCACCATGG
328 V  A  L  K  S  Y  E  E  E  L  A  K  D  P  R  I  A  A  T  M

                                                  Factor Xa  PstI
   AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGCCTCGG
348 E  N  A  Q  S  A  F  W  Y  A  V  R  I  E  A  R  L  Q  A  S

    SalI        XbaI              FLAG                Lost XbaI
    TCGACGCCGAATCTAGAGATTATAAAGATGACGATGACAAATAATAAGCTAGAGG
60  (trxn stop)
```

```
368      V  D  A  E  S  R  D  Y  K  D  D  D  D  K
```

pMPX-86::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG
Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-86 cut with PstI & XbaI.

SEQ ID NO.: 274

pMPX-79 TrxA (2-109 del 103-107) fusion vector

```
                        SD      PstI          SalI          XbaI  +2 trxA(del
103-107)
1             TAGCAGGAGGCCCTGCAGGCCTCGGTCGACGCCGAATCTAGAAGCGATAAAATTATT
1                                  A  S  V  D  A  E  S  R  S  D  K  I  I

61         CACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTC
17          H  L  T  D  D  S  F  D  T  D  V  L  K  A  D  G  A  I  L  V

121        GATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGAAATC
37          D  F  W  A  E  W  C  G  P  C  K  M  I  A  P  I  L  D  E  I

181        GCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAACATCGATCAAAACCCTGGC
57          A  D  E  Y  Q  G  K  L  T  V  A  K  L  N  I  D  Q  N  P  G

241        ACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACGGTGAA
77          T  A  P  K  Y  G  I  R  G  I  P  T  L  L  L  F  K  N  G  E

301        GTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGGCGGAT
97          V  A  A  T  K  V  G  A  L  S  K  G  Q  L  K  E  N  L  A  D

                  FLAG                Lost XbaI
361        TATAAAGATGACGATGACAAATAATAAGCTAGAGG  (transcriptional stop)
117         Y  K  D  D  D  D  K
```

pMPX-71::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG
Arabinose inducible, clone into PstI, SalI, XbaI
+1 Met required for protein to be fused

Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-NheI insertion with PstI & NheI and cloning into pMPX-71 cut with PstI & XbaI.

SEQ ID NO.: 275

pMPX-78 TrxA (2-109 del 103-107) fusion vector

```
                                                              SD      PstI
1             GAATTCAGGCGCTTTTTAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCAGGCCTC
1                                                                    A  S
```

```
                SalI        XbaI  +2 trxA(del 103-107)
61      GGTCGACGCCGAATCTAGAAGCGATAAAATTATTCACCTGACTGACGACAGTTTTGACAC
6         V  D  A  E  S  R  S  D  K  I  I  H  L  T  D  D  S  F  D  T

121     GGATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCC
26        D  V  L  K  A  D  G  A  I  L  V  D  F  W  A  E  W  C  G  P

181     GTGCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAACTGAC
46        C  K  M  I  A  P  I  L  D  E  I  A  D  E  Y  Q  G  K  L  T

241     CGTTGCAAAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGG
66        V  A  K  L  N  I  D  Q  N  P  G  T  A  P  K  Y  G  I  R  G

301     TATCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACT
86        I  P  T  L  L  L  F  K  N  G  E  V  A  A  T  K  V  G  A  L

                                                      FLAG

361
GTCTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAATAATAA
106       S  K  G  Q  L  K  E  N  L  A  D  Y  K  D  D  D  D  K

          lost XbaI
          GCTAGAGG  (transcriptional stop)
```

pMPX-72::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG
Rhamnose inducible, clone into PstI, SalI, XbaI
+1 Met required for protein to be fused

Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-NheI insertion with PstI & NheI and cloning into pMPX-72 cut with PstI & XbaI.

SEQ ID NO.: 276

pMPX-90 TrxA (2-109 del 103-107) fusion vector

```
                    SD      PstI          SalI          XbaI  +2 trxA(del
103-107)
                AGGAGGTTCTGCAGGCCTCGGTCGACGCCGAATCTAGAAGCGATAAAATTATT
1                                 A  S  V  D  A  E  S  R  S  D  K  I  I

          CACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTC
17         H  L  T  D  D  S  F  D  T  D  V  L  K  A  D  G  A  I  L  V

          GATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGAAATC
37         D  F  W  A  E  W  C  G  P  C  K  M  I  A  P  I  L  D  E  I

          GCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAACATCGATCAAAACCCTGGC
57         A  D  E  Y  Q  G  K  L  T  V  A  K  L  N  I  D  Q  N  P  G

          ACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACGGTGAA
77         T  A  P  K  Y  G  I  R  G  I  P  T  L  L  L  F  K  N  G  E

          GTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGGCGGAT
97         V  A  A  T  K  V  G  A  L  S  K  G  Q  L  K  E  N  L  A  D

                    FLAG                Lost XbaI
```

TATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC (transcriptional stop)
117 Y K D D D D K

pMPX-84::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG
Temperature inducible, clone into PstI, SalI, XbaI
+1 Met required for protein to be fused

Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-NheI insertion with PstI & NheI and cloning into pMPX-84 cut with PstI & XbaI.

SEQ ID NO.: 277

pMPX-95 TrxA (2-109 del 103-107) fusion vector

SD PstI SalI XbaI +2 trxA(del 103-107)
AGGAGGTTCTGCAGGCCTCGGTCGACGCCGAATCTAGAAGCGATAAAATTATT
1 A S V D A E S R S D K I I

CACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTC
17 H L T D D S F D T D V L K A D G A I L V

GATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGAAATC
37 D F W A E W C G P C K M I A P I L D E I

GCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAACATCGATCAAAACCCTGGC
57 A D E Y Q G K L T V A K L N I D Q N P G

ACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACGGTGAA
77 T A P K Y G I R G I P T L L L F K N G E

GTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGGCG**GAT**
97 V A A T K V G A L S K G Q L K E N L A D

FLAG Lost XbaI
TATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC (transcriptional stop)
117 Y K D D D D K

pMPX-86::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG
Temperature inducible, clone into PstI, SalI, XbaI
+1 Met required for protein to be fused

Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-NheI insertion with PstI & NheI and cloning into pMPX-86 cut with PstI & XbaI.

SEQ ID NO.: 278

pMPX-80 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1
malE(1-28)
2401 GAATTCAGGCGCTTTTTAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCATATGAAAAT

```
1                                                                  M  K  I

2461    AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTC
4         K  T  G  A  R  I  L  A  L  S  A  L  T  T  M  M  F  S  A  S

                              Factor Xa   PstI        SalI        XbaI
2521    GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCTAGAAG
24        A  L  A  K  I  I  E  A  R  L  Q  A  S  V  D  A  E  S  R  S

      +2 trxA (2-109 del 103-107)
2581    CGATAAAATTATTCACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGG
44        D  K  I  I  H  L  T  D  D  S  F  D  T  D  V  L  K  A  D  G

2641    GGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGAT
64        A  I  L  V  D  F  W  A  E  W  C  G  P  C  K  M  I  A  P  I

2701    TCTGGATGAAATCGCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAACATCGA
84        L  D  E  I  A  D  E  Y  Q  G  K  L  T  V  A  K  L  N  I  D

2761    TCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTT
104       Q  N  P  G  T  A  P  K  Y  G  I  R  G  I  P  T  L  L  L  F

2821    CAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGA
124       K  N  G  E  V  A  A  T  K  V  G  A  L  S  K  G  Q  L  K  E

                                FLAG                Lost XbaI
2881    GAACCTGGCGGATTATAAAGATGACGATGACAAATAATAAGCTAGAGG (trxn stop)
144       N  L  A  D  Y  K  D  D  D  D  K
```

pMPX-72::malE(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG
Rhamnose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-78 cut with PstI & XbaI.

SEQ ID NO.: 279

pMPX-81 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

```
                                        SD  Lost PstI +1 malE (1-28)
1621    CCATACCCGTTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAAACAGGTGCAC
1                                                 M  K  I  K  T  G  A

1681    GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCCAAAA
8       R  I  L  A  L  S  A  L  T  T  M  M  F  S  A  S  A  L  A  K

                                                          +2 trxA(2-109
      del          Factor Xa   PstI        SalI        XbaI
      103-107)
1741    TCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCTAGAAGCGATAAAATTATTC
28      I  I  E  A  R  L  Q  A  S  V  D  A  E  S  R  S  D  K  I  I

1801    ACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTCG
48      H  L  T  D  D  S  F  D  T  D  V  L  K  A  D  G  A  I  L  V

1861    ATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGAAATCG
68      D  F  W  A  E  W  C  G  P  C  K  M  I  A  P  I  L  D  E  I
```

```
1921    CTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAACATCGATCAAAACCCTGGCA
88      A  D  E  Y  Q  G  K  L  T  V  A  K  L  N  I  D  Q  N  P  G

1981    CTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACGGTGAAG
108     T  A  P  K  Y  G  I  R  G  I  P  T  L  L  L  F  K  N  G  E

2041    TGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGGCGGATT
128     V  A  A  T  K  V  G  A  L  S  K  G  Q  L  K  E  N  L  A  D

                FLAG
2101    ATAAAGATGACGATGACAAATAATAAGCTAGAGG  (transcriptional stop)
148     Y  K  D  D  D  D  K
```

pMPX-71::malE(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG
Arabinose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-79 cut with PstI & XbaI.

SEQ ID NO.: 280

pMPX-91 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

```
                                                    SD  Lost PstI +1
malE(1-28)
                                                    AGGAGGTTCTGCATATGAAAAT
1                                                                M  K  I

          AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTC
4           K  T  G  A  R  I  L  A  L  S  A  L  T  T  M  M  F  S  A  S

                          Factor Xa   PstI        SalI        XbaI
          GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCTAGAAG
24          A  L  A  K  I  I  E  A  R  L  Q  A  S  V  D  A  E  S  R  S

                    +2 trxA (2-109 del 103-107)

          CGATAAAATTATTCACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGG
44          D  K  I  I  H  L  T  D  D  S  F  D  T  D  V  L  K  A  D  G

          GGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGAT
64          A  I  L  V  D  F  W  A  E  W  C  G  P  C  K  M  I  A  P  I

          TCTGGATGAAATCGCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAACATCGA
84          L  D  E  I  A  D  E  Y  Q  G  K  L  T  V  A  K  L  N  I  D

          TCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTT
104         Q  N  P  G  T  A  P  K  Y  G  I  R  G  I  P  T  L  L  L  F

          CAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGA
124         K  N  G  E  V  A  A  T  K  V  G  A  L  S  K  G  Q  L  K  E

                              FLAG                Lost XbaI
          GAACCTGGCGGATTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC (trxn
stop)
```

144 N L A D Y K D D D D K

pMPX-84::malE(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG
Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-90 cut with PstI & XbaI.

SEQ ID NO.: 281

pMPX-96 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1

malE(1-28)

AGGAGGTTCTGCATATGAAAAT
1 M K I

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTC
4 K T G A R I L A L S A L T T M M F S A S

Factor Xa PstI SalI XbaI
GGCTCTCGCCAAAATC**ATCGAAGCCCGC**CTGCAGGCCTCGGTCGACGCCGAATCTAGAAG
24 A L A K I I E A R L Q A S V D A E S R S

+2 trxA (2-109 del 103-107)
CGATAAAATTATTCACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGG
44 D K I I H L T D D S F D T D V L K A D G

GGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGAT
64 A I L V D F W A E W C G P C K M I A P I

TCTGGATGAAATCGCTGACGAATATCAGGGCAAACTGACCGTTGCAAAACTGAACATCGA
84 L D E I A D E Y Q G K L T V A K L N I D

TCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTT
104 Q N P G T A P K Y G I R G I P T L L L F

CAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGA
124 K N G E V A A T K V G A L S K G Q L K E

FLAG Lost XbaI
GAACCTGGCG**GATTATAAAGATGACGATGACAAA**TAATAAGCTAGAGGTACC (trxn stop)
144 N L A D Y K D D D D K

pMPX-86::malE(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG
Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-95 cut with PstI & XbaI.

SEQ ID NO.: 282

pMPX-83 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

```
                                                        SD  Lost PstI +1
malE(1-28)
2401    GAATTCAGGCGCTTTTTAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCATATGAAAAT
1                                                                M  K  I

2461    AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTC
4         K  T  G  A  R  I  L  A  L  S  A  L  T  T  M  M  F  S  A  S

2521    GGCTCTCGCCAAAATCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTA
24        A  L  A  K  I  E  E  G  K  L  V  I  W  I  N  G  D  K  G  Y

2581    TAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGT
44        N  G  L  A  E  V  G  K  K  F  E  K  D  T  G  I  K  V  T  V

2641    TGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCC
64        E  H  P  D  K  L  E  E  K  F  P  Q  V  A  A  T  G  D  G  P

2701    TGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGC
84        D  I  I  F  W  A  H  D  R  F  G  G  Y  A  Q  S  G  L  L  A

2761    TGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGT
104       E  I  T  P  D  K  A  F  Q  D  K  L  Y  P  F  T  W  D  A  V

2821    ACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTA
124       R  Y  N  G  K  L  I  A  Y  P  I  A  V  E  A  L  S  L  I  Y

2881    TAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAA
144       N  K  D  L  L  P  N  P  P  K  T  W  E  E  I  P  A  L  D  K

2941    AGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCAC
164       E  L  K  A  K  G  K  S  A  L  M  F  N  L  Q  E  P  Y  F  T

3001    CTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGA
184       W  P  L  I  A  A  D  G  G  Y  A  F  K  Y  E  N  G  K  Y  D

3061    CATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGA
204       I  K  D  V  G  V  D  N  A  G  A  K  A  G  L  T  F  L  V  D

3121    CCTGATTAAAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTT
224       L  I  K  N  K  H  M  N  A  D  T  D  Y  S  I  A  E  A  A  F

3181    TAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACAC
244       N  K  G  E  T  A  M  T  I  N  G  P  W  A  W  S  N  I  D  T

3241    CAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACC
264       S  K  V  N  Y  G  V  T  V  L  P  T  F  K  G  Q  P  S  K  P

3301    GTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAA
284       F  V  G  V  L  S  A  G  I  N  A  A  S  P  N  K  E  L  A  K

3361    AGAGTTCCTCGAAAACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAA
304       E  F  L  E  N  Y  L  L  T  D  E  G  L  E  A  V  N  K  D  K

3421    ACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTAT
324       P  L  G  A  V  A  L  K  S  Y  E  E  E  L  A  K  D  P  R  I
```

```
                                                                  Factor Xa
3481    TGCCGCCACCATGGAAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCG
344       A  A  T  M  E  N  A  Q  S  A  F  W  Y  A  V  R  I  E  A  R

          PstI        SalI        XbaI  +2 trxA (2-109 del 103-107)
3541    CCTGCAGGCCTCGGTCGACGCCGAATCTAGAAGCGATAAAATTATTCACCTGACTGACGA
364       L  Q  A  S  V  D  A  E  S  R  S  D  K  I  I  H  L  T  D  D

3601    CAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGA
384       S  F  D  T  D  V  L  K  A  D  G  A  I  L  V  D  F  W  A  E

3661    GTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCA
404       W  C  G  P  C  K  M  I  A  P  I  L  D  E  I  A  D  E  Y  Q

3721    GGGCAAACTGACCGTTGCAAAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATA
424       G  K  L  T  V  A  K  L  N  I  D  Q  N  P  G  T  A  P  K  Y

3781    TGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAA
444       G  I  R  G  I  P  T  L  L  L  F  K  N  G  E  V  A  A  T  K

                                                                  FLAG
3841    AGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGA
464       V  G  A  L  S  K  G  Q  L  K  E  N  L  A  D  Y  K  D  D  D

3901    TGACAAATAATAAGCTAGAGG  (transcriptional stop)
484       D  K
```

pMPX-72::malE(1-320 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG
Rhamnose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-78 cut with PstI & XbaI.

SEQ ID NO.: 283

pMPX-82 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

```
                                          SD  Lost PstI +1 malE (1-370 del
352-362)
1621    CCATACCCGTTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAAACAGGTGCAC
1                                                 M  K  I  K  T  G  A

1681    GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCCAAAA
8       R  I  L  A  L  S  A  L  T  T  M  M  F  S  A  S  A  L  A  K

1741    TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCTCGCTG
28      I  E  E  G  K  L  V  I  W  I  N  G  D  K  G  Y  N  G  L  A

1801    AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCCGGATA
48      E  V  G  K  K  F  E  K  D  T  G  I  K  V  T  V  E  H  P  D

1861    AACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCT
68      K  L  E  E  K  F  P  Q  V  A  A  T  G  D  G  P  D  I  I  F

1921    GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGG
88      W  A  H  D  R  F  G  G  Y  A  Q  S  G  L  L  A  E  I  T  P
```

```
1981    ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAACGGCA
108     D  K  A  F  Q  D  K  L  Y  P  F  T  W  D  A  V  R  Y  N  G

2041    AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGATCTGC
128     K  L  I  A  Y  P  I  A  V  E  A  L  S  L  I  Y  N  K  D  L

2101    TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGAAAGCGA
148     L  P  N  P  P  K  T  W  E  E  I  P  A  L  D  K  E  L  K  A

2161    AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCTGATTG
168     K  G  K  S  A  L  M  F  N  L  Q  E  P  Y  F  T  W  P  L  I

2221    CTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGACGTGG
188     A  A  D  G  G  Y  A  F  K  Y  E  N  G  K  Y  D  I  K  D  V

2281    GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAAAAACA
208     G  V  D  N  A  G  A  K  A  G  L  T  F  L  V  D  L  I  K  N

2341    AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAA
228     K  H  M  N  A  D  T  D  Y  S  I  A  E  A  A  F  N  K  G  E

2401    CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTGAATT
248     T  A  M  T  I  N  G  P  W  A  W  S  N  I  D  T  S  K  V  N

2461    ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGGCGTGC
268     Y  G  V  T  V  L  P  T  F  K  G  Q  P  S  K  P  F  V  G  V

2521    TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCTCGAAA
288     L  S  A  G  I  N  A  A  S  P  N  K  E  L  A  K  E  F  L  E

2581    ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGGTGCCG
308     N  Y  L  L  T  D  E  G  L  E  A  V  N  K  D  K  P  L  G  A

2641    TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCACCATGG
328     V  A  L  K  S  Y  E  E  E  L  A  K  D  P  R  I  A  A  T  M

                                                  Factor Xa   PstI
2701    AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGCCTCGG
348     E  N  A  Q  S  A  F  W  Y  A  V  R  I  E  A  R  L  Q  A  S

        SalI          XbaI  +2 trxA (2-109 del 103-107)
2761    TCGACGCCGAATCTAGAAGCGATAAAATTATTCACCTGACTGACGACAGTTTTGACACGG
368     V  D  A  E  S  R  S  D  K  I  I  H  L  T  D  D  S  F  D  T

2821    ATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGT
388     D  V  L  K  A  D  G  A  I  L  V  D  F  W  A  E  W  C  G  P

2881    GCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAACTGACCG
408     C  K  M  I  A  P  I  L  D  E  I  A  D  E  Y  Q  G  K  L  T

2941    TTGCAAAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTA
428     V  A  K  L  N  I  D  Q  N  P  G  T  A  P  K  Y  G  I  R  G

3001    TCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGT
448     I  P  T  L  L  L  F  K  N  G  E  V  A  A  T  K  V  G  A  L

                                                      FLAG
3061    CTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAATAATAAG
468     S  K  G  Q  L  K  E  N  L  A  D  Y  K  D  D  D  D  K
```

Lost XbaI
CTAGAGG (transcriptional stop)

pMPX-71::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG
Arabinose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-79 cut with PstI & XbaI.

SEQ ID NO.: 284

pMPX-92 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

```
                                                SD  Lost PstI +1 malE (1-370 del
354-364)
                                                AGGAGGTTCTGCATATGAAAATAAAAACAGGTGCAC
1                                                           M  K  I  K  T  G  A

               GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCCAAAA
8              R  I  L  A  L  S  A  L  T  T  M  M  F  S  A  S  A  L  A  K

               TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCTCGCTG
28             I  E  E  G  K  L  V  I  W  I  N  G  D  K  G  Y  N  G  L  A

               AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCCGGATA
48             E  V  G  K  K  F  E  K  D  T  G  I  K  V  T  V  E  H  P  D

               AACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCT
68             K  L  E  E  K  F  P  Q  V  A  A  T  G  D  G  P  D  I  I  F

               GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGG
88             W  A  H  D  R  F  G  G  Y  A  Q  S  G  L  L  A  E  I  T  P

               ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAACGGCA
108            D  K  A  F  Q  D  K  L  Y  P  F  T  W  D  A  V  R  Y  N  G

               AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGATCTGC
128            K  L  I  A  Y  P  I  A  V  E  A  L  S  L  I  Y  N  K  D  L

               TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGAAAGCGA
148            L  P  N  P  P  K  T  W  E  E  I  P  A  L  D  K  E  L  K  A

               AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCTGATTG
168            K  G  K  S  A  L  M  F  N  L  Q  E  P  Y  F  T  W  P  L  I

               CTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGACGTGG
188            A  A  D  G  G  Y  A  F  K  Y  E  N  G  K  Y  D  I  K  D  V

               GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAAAAACA
208            G  V  D  N  A  G  A  K  A  G  L  T  F  L  V  D  L  I  K  N

2341           AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAA
228            K  H  M  N  A  D  T  D  Y  S  I  A  E  A  A  F  N  K  G  E
```

```
2401    CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTGAATT
248     T  A  M  T  I  N  G  P  W  A  W  S  N  I  D  T  S  K  V  N

2461    ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGGCGTGC
268     Y  G  V  T  V  L  P  T  F  K  G  Q  P  S  K  P  F  V  G  V

2521    TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCTCGAAA
288     L  S  A  G  I  N  A  A  S  P  N  K  E  L  A  K  E  F  L  E

2581    ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGGTGCCG
308     N  Y  L  L  T  D  E  G  L  E  A  V  N  K  D  K  P  L  G  A

2641    TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCACCATGG
328     V  A  L  K  S  Y  E  E  E  L  A  K  D  P  R  I  A  A  T  M

                                                  Factor Xa   PstI
2701    AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGCCTCGG
348     E  N  A  Q  S  A  F  W  Y  A  V  R  I  E  A  R  L  Q  A  S

        SalI          XbaI  +2 trxA (2-109 del 103-107)
2761    TCGACGCCGAATCTAGAAGCGATAAAATTATTCACCTGACTGACGACAGTTTTGACACGG
368     V  D  A  E  S  R  S  D  K  I  I  H  L  T  D  D  S  F  D  T

2821    ATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGT
388     D  V  L  K  A  D  G  A  I  L  V  D  F  W  A  E  W  C  G  P

2881    GCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAACTGACCG
408     C  K  M  I  A  P  I  L  D  E  I  A  D  E  Y  Q  G  K  L  T

2941    TTGCAAAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTA
428     V  A  K  L  N  I  D  Q  N  P  G  T  A  P  K  Y  G  I  R  G

3001    TCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGT
448     I  P  T  L  L  L  F  K  N  G  E  V  A  A  T  K  V  G  A  L

                                                    FLAG
3061    CTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAATAATAAG
468     S  K  G  Q  L  K  E  N  L  A  D  Y  K  D  D  D  D  K

      Lost XbaI
        CTAGAGGTACC (transcriptional stop)
```

pMPX-84::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG
Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-90 cut with PstI & XbaI.

SEQ ID NO.: 285

pMPX-97 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

```
                                        SD  Lost PstI +1 malE (1-370 del
354-364)
                                      AGGAGGTTCTGCATATGAAAATAAAAACAGGTGCAC
```

```
     1                                                        M  K  I  K  T  G  A

          GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCCAAAA
     8    R  I  L  A  L  S  A  L  T  T  M  M  F  S  A  S  A  L  A  K
5
          TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCTCGCTG
    28    I  E  E  G  K  L  V  I  W  I  N  G  D  K  G  Y  N  G  L  A

          AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCCGGATA
10  48    E  V  G  K  K  F  E  K  D  T  G  I  K  V  T  V  E  H  P  D

          AACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCT
    68    K  L  E  E  K  F  P  Q  V  A  A  T  G  D  G  P  D  I  I  F

15        GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGG
    88    W  A  H  D  R  F  G  G  Y  A  Q  S  G  L  L  A  E  I  T  P

          ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAACGGCA
   108    D  K  A  F  Q  D  K  L  Y  P  F  T  W  D  A  V  R  Y  N  G
20
          AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGATCTGC
   128    K  L  I  A  Y  P  I  A  V  E  A  L  S  L  I  Y  N  K  D  L

          TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGAAAGCGA
25  148    L  P  N  P  P  K  T  W  E  E  I  P  A  L  D  K  E  L  K  A

          AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCTGATTG
   168    K  G  K  S  A  L  M  F  N  L  Q  E  P  Y  F  T  W  P  L  I

30        CTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGACGTGG
   188    A  A  D  G  G  Y  A  F  K  Y  E  N  G  K  Y  D  I  K  D  V

          GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAAAAACA
   208    G  V  D  N  A  G  A  K  A  G  L  T  F  L  V  D  L  I  K  N
35
  2341    AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAA
   228    K  H  M  N  A  D  T  D  Y  S  I  A  E  A  A  F  N  K  G  E

  2401    CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTGAATT
40 248    T  A  M  T  I  N  G  P  W  A  W  S  N  I  D  T  S  K  V  N

  2461    ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGGCGTGC
   268    Y  G  V  T  V  L  P  T  F  K  G  Q  P  S  K  P  F  V  G  V

45 2521    TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCTCGAAA
   288    L  S  A  G  I  N  A  A  S  P  N  K  E  L  A  K  E  F  L  E

  2581    ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGGTGCCG
   308    N  Y  L  L  T  D  E  G  L  E  A  V  N  K  D  K  P  L  G  A
50
  2641    TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCACCATGG
   328    V  A  L  K  S  Y  E  E  E  L  A  K  D  P  R  I  A  A  T  M

                                                  Factor Xa   PstI
55 2701    AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGCCTCGG
   348    E  N  A  Q  S  A  F  W  Y  A  V  R  I  E  A  R  L  Q  A  S

          SalI        XbaI  +2 trxA (2-109 del 103-107)
  2761    TCGACGCCGAATCTAGAAGCGATAAAATTATTCACCTGACTGACGACAGTTTTGACACGG
60 368    V  D  A  E  S  R  S  D  K  I  I  H  L  T  D  D  S  F  D  T
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2821    ATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGT
388     D  V  L  K  A  D  G  A  I  L  V  D  F  W  A  E  W  C  G  P

2881    GCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAACTGACCG
408     C  K  M  I  A  P  I  L  D  E  I  A  D  E  Y  Q  G  K  L  T

2941    TTGCAAAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTA
428     V  A  K  L  N  I  D  Q  N  P  G  T  A  P  K  Y  G  I  R  G

3001    TCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGT
448     I  P  T  L  L  L  F  K  N  G  E  V  A  A  T  K  V  G  A  L

                                                    FLAG
3061    CTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAATAATAAG
468     S  K  G  Q  L  K  E  N  L  A  D  Y  K  D  D  D  D  K
```

Lost XbaI
CTAGAGGTACC (transcriptional stop)

pMPX-86::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-95 cut with PstI & XbaI.